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For the President of the European Patent Office

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Methods and nucleic acids for the analysis of CpG dinucleotide methylation status
associated with the development of prostate cancer

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**METHODS AND NUCLEIC ACIDS FOR THE ANALYSIS OF CpG
DINUCLEOTIDE METHYLATION STATUS ASSOCIATED WITH THE
DEVELOPMENT OF PROSTATE CANCER**

FIELD OF THE INVENTION

The present invention relates to human DNA sequences that exhibit altered methylation patterns (hypermethylation or hypomethylation) in prostate cancer patients. Particular embodiments of the invention provide highly accurate methods for detection and differentiation of prostate carcinomas.

BACKGROUND

Correlation of aberrant DNA methylation with cancer. Aberrant DNA methylation within CpG 'islands' is characterized by *hyper-* or *hypomethylation* of CpG dinucleotide sequences leading to abrogation or over expression of a broad spectrum of genes, and is among the earliest and most common alterations found in, and correlated with human malignancies. Additionally, abnormal methylation has been shown to occur in CpG-rich regulatory elements in both intronic and coding parts of genes for certain tumors. In colon cancer, aberrant DNA methylation constitutes one of the most prominent alterations and inactivates many tumor suppressor genes including, *inter alia*, p14ARF, p16INK4a, THBS1, MINT2, and MINT31 and DNA mismatch repair genes such as hMLH1.

Aside from the specific hypermethylation of tumor suppressor genes, an overall hypomethylation of DNA can be observed in tumor cells. This decrease in global methylation can be detected early, far before the development of frank tumor formation. A correlation between hypomethylation and increased gene expression has been determined for many oncogenes.

Prostate cancer. Prostate cancer is the most common malignancy among men in the United States (~200,000 new cases per year), and the sixth leading cause of male cancer-related

deaths worldwide (~204,000 per year) . Prostate cancer is primarily a disease of the elderly, with approximately 16% of men between the ages of 60 and 79 having the disease. According to some estimates at autopsy, 80% of all men over 80 years of age have some form of prostate disease (eg cancer, BPH, prostatitis, etc). Benign prostate hypertrophy is present in about 50% of men aged 50 or above, and in 95% of men aged 75 or above. It is obvious from these reports that prostate cancer is often not a disease that men die from, but with. Recent evidence suggests that the incidence of prostate cancer may in fact be declining, likely as result of better treatment, better surgery, and earlier detection.

Diagnosis and prognosis of prostate cancer; deficiencies of prior art approaches. Current guidelines for prostate cancer screening have been suggested by the American Cancer Society and are as follows: At 50 years of age, health care professionals should offer a blood test for prostate specific antigen (PSA) and perform a digital rectal exam (DRE). It is recommended that high risk populations, such as African Americans and those with a family history of prostate disease, should begin screening at 45 years of age. Men without abnormal prostate pathology generally have a PSA level in blood below 4ng/ml. PSA levels between 4ng/ml and 10ng/ml (called the „Grey Zone“) have a 25% chance of having prostate cancer. The result is that 75% of the time, men with an abnormal DRE and a PSA in this grey zone have a negative, or a seemingly unnecessary biopsy. Above the grey zone, the likelihood of having prostate cancer is significant (> 67%) and increases even further as PSA levels go up. Numerous methods exist for measuring PSA (percent-free PSA, PSA velocity, PSA density, etc.), and each has an associated accuracy for detecting the presence of cancer. Yet, even with the minor improvements in detection, and the reported drops in mortality associated with screening, the frequency of false positives remains high. Reduced specificity results in part from increased blood PSA associated with BPH, and prostatitis. It has also been estimated that up to 45% of prostate biopsies under current guidelines are falsely negative, resulting in decreased sensitivity even with biopsy.

TRUS guided biopsy is considered the gold standard for diagnosing prostate cancer.

Recommendations for biopsy are based upon abnormal PSA levels and or an abnormal DREs. For PSA there is a grey zone where a high percentage of biopsies are perhaps not necessary. Yet the ability to detect cancer in this grey zone (PSA levels of 4.0 to 10 ng/ml) is difficult without biopsy. Due to this lack of specificity, 75% of men undergoing a biopsy do not have cancer (25). Yet without biopsy, those with cancer would be missed, resulting in increased morbidity and mortality. However the risks associated with an unnecessary biopsy are also high.

It is clear that there is a need for an early, specific prostate cancer test for more accurate detection and treatment monitoring, to improve morbidity and mortality rates. However, using routine histological examination, it is often difficult to distinguish benign hyperplasia of the prostate from early stages of prostate carcinoma, even if an adequate biopsy is obtained (McNeal J. E. et al., *Hum. Pathol.* 2001, 32:441-6). Furthermore, small or otherwise insufficient biopsy samples often impede the analysis.

Molecular markers would offer the advantage that they could be used to efficiently analyze even very small tissue samples, and samples whose tissue architecture has not been maintained. Within the last decade, numerous genes have been studied with respect to differential expression among benign hyperplasia of the prostate and different grades of prostate cancer. However, no single marker has as yet been shown to be sufficient for the diagnosis of prostate tumors in a clinical setting.

Alternatively, high-dimensional mRNA-based approaches may, in particular instances, provide a means to distinguish between different tumor types and benign and malignant lesions. However, application of such approaches as a routine diagnostic tool in a clinical environment is impeded and substantially limited by the extreme instability of mRNA, the rapidly occurring expression changes following certain triggers (e.g., sample collection), and, most importantly, by the large amount of mRNA needed for analysis which often cannot be obtained from a routine biopsy (see, e.g., Lipshutz, R. J. et al., *Nature Genetics* 21:20-24, 1999; Bowtell, D. D. L. *Nature Genetics Suppl.* 21:25-32, 1999).

The GSTP1 gene. The core promoter region of the Glutathione S-Transferase P gene (GSTP1; accession no. NM_000852) has been shown to be hypermethylated in prostate tumor tissue. The glutathione S-transferase pi enzyme is involved in the detoxification of electrophilic carcinogens, and impaired or decreased levels of enzymatic activity (GSTP1 impairment) have been associated with the development of neoplasms, particularly in the prostate. Mechanisms of GSTP1 impairment include mutation (the GSTP*B allele has been associated with a higher risk of cancer) and methylation.

Prior art GSTP1 studies. Lee et al., in United States Patent No 5,552,277, disclosed that the expression of the glutathione-S-transferase (GST) Pi gene was downregulated in a significant proportion of prostate carcinomas. Moreover, by means of restriction enzyme analysis they were able to show that the promoter region of the of the GSTP1 gene was upmethyalted (hypermethylated) in prostate carcinomas as opposed to normal prostate and leukocyte tissue. However, due to the limited and imprecise nature of the analysis technique

used (HpaIII digestion, followed by Southern blotting) the exact number and position of the methylated CG dinucleotides were not characterized.

Douglas et al. (WO9955905) used a method comprising bisulfite treatment, followed by methylation specific PCR to show that prostate carcinoma-specific GSTP1 hypermethylation was localized to the core promoter regions, and localized a number of CpG positions that had not been characterised by Lee et al.

Herman and Baylin (United States Patent No. 6,017,704) describe the use of methylation specific primers for methylation analysis, and describe a particular primer pair suitable for the analysis of the corresponding methylated GSTP1 promoter sequence.

However, with respect to the use of GSTP1 markers, the prior art is limited with respect to the number of GSTP1 promoter CpG sequences that have been characterized for differential methylation status. Moreover, there are no disclosures, suggestions or teachings in the prior art of how such markers could be used to distinguish among benign hyperplasia of the prostate and different grades of prostate cancer. Furthermore, GSTP1 has been shown to be methylated in other cancers. For this reason it is critical to identify markers other than GSTP1 that have high performance values in the prostate, but not other organs.

Aberrant genetic methylation in prostate cancer has also been observed in several other genes including AR, p16 (CDKN2a/INK4a), CD44, CDH1. Genome wide hypomethylation for example of the LINE-1 repetitive element has also been associated with tumor progression (Santourlidis S, Florl A, Ackermann R, Wirtz HC, Schulz WA 'High frequency of alterations in DNA methylation in adenocarcinoma of the prostate.' Prostate 1999 May 15; 39(3): 166-74).

However, use of these genes as alternative or supplemental diagnostic, or otherwise clinically useful markers in a commercial setting has not been enabled. The application of differentially methylated genes to clinically utilizable platforms requires much further investigation into the sensitivity and specificity of the genes. For example, in the case of the gene CD44, a known metastasis suppressor, downregulation was associated with hypermethylation. However the use of this gene as a commercially available marker was not enabled as it was also methylated in normal tissues. See Vis AN, Oomen M, Schroder FH, van der Kwast TH 'Feasibility of assessment of promoter methylation of the CD44 gene in serum of prostate cancer patients.' Mol Urol. 2001 Winter;5(4):199-203.

Pronounced need in the art. Therefore, in view of the incidence of prostate hyperplasia (50% of men aged 50 or above, and 95% of men aged 75 or above) and prostate cancer (180 per 100,000), there is a substantial need in the art for the development of

molecular markers that could be used to effectively detect prostate cell proliferative disorders, in particular prostate carcinoma. There is also a particular need in the art for a means of distinguishing benign hyperplasia of the prostate and prostate cancer. Additionally, there is a pronounced need in the art for the development of molecular markers that could be used to provide sensitive, accurate and non-invasive methods (as opposed to, e.g., biopsy and transrectal ultrasound) for the diagnosis of and differentiation between prostate cell proliferative disorders.

SUMMARY OF THE INVENTION

The present invention provides a method for ascertaining genetic and/or epigenetic parameters of genomic DNA. The method has utility for the improved diagnosis, treatment and monitoring of prostate cell proliferative disorders, more specifically by enabling the improved identification of and differentiation between subclasses of said disorder and the genetic predisposition to said disorders. The present invention provides novel methods for detecting and/or distinguishing between prostate cell proliferative disorders. The invention provides methods for the analysis of biological samples for features associated with the development of prostate cell proliferative disorders, in particular benign prostate hyperplasia (hereinafter also referred to as BPH) and prostate carcinoma, the method thereby enables the early detection of prostate carcinomas and their differentiation from benign cell proliferative disorders of the prostate, including BPH. The method is characterised in that at least one nucleic acid, or a fragment thereof, from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 295 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence, or sequences of interest.

In a particularly preferred embodiment said method enables the differentiation between non-cancerous types of prostate tissue (including BPH and normal) and prostate carcinoma. In a further embodiment the method enables the differentiation of prostate cancer from normal prostate tissue, tissues originating from other tissues and BPH. In a further embodiment the method enables the differentiation of prostate cancer from cancers originating from other tissues. The invention presents improvements over the state of the art in that it enables a highly specific classification of prostate cell proliferative disorders, thereby allowing for improved and informed treatment of patients. In particular it allows for the differentiation of BPH from prostate carcinoma. The invention provides further improvements

over the state of the art in that said method may be used for the analysis of bodily fluids including post prostatic massage urine, ejaculate, urine, or blood, it therefore enables a non invasive means for the detection and/or differentiation of prostate cell proliferative disorders.

Preferably, the source of the test sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. More preferably, the source is bodily fluids, post prostatic massage urine, ejaculate, urine, or blood.

Specifically, the present invention provides a method for detecting prostate cell proliferative disorders, comprising: obtaining a biological sample comprising genomic nucleic acid(s); contacting the nucleic acid(s), or a fragment thereof, with one reagent or a plurality of reagents sufficient for distinguishing between methylated and non-methylated CpG dinucleotide sequences within at least one target sequence of the subject nucleic acid, wherein the target sequence comprises, or hybridizes under stringent conditions to, a sequence comprising at least 16 contiguous nucleotides of at least one sequence taken from the group consisting SEQ ID NO: 1 to 295, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence; and determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences. Preferably, distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises methylation state-dependent conversion or non-conversion of at least one such CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and contiguous regions thereof corresponding to the target sequence.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences

according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Additional embodiments provide a method for the detection of prostate cell proliferative disorders, comprising: obtaining a biological sample having subject genomic DNA; extracting the genomic DNA; treating the genomic DNA, or a fragment thereof, with one or more reagents to convert 5-position unmethylated cytosine bases to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties; contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, wherein the treated DNA or the fragment thereof is either amplified to produce an amplificate, or is not amplified; and determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 , or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences thereof.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes to, one or

more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Preferably, at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase. Preferably, determining comprises use of at least two methods selected from the group consisting of: hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule, bound to a solid phase, comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing of the amplificate.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

For all said embodiments the following embodiments are particularly preferred. Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the target sequence(s) comprise, or hybridizes under stringent conditions to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Further embodiments provide a method for the analysis of prostate cell proliferative disorders, comprising: obtaining a biological sample having subject genomic DNA; extracting the genomic DNA; contacting the genomic DNA, or a fragment thereof, comprising one or more sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 or a sequence that hybridizes under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is either digested thereby to produce digestion fragments, or is not digested thereby; and determining, based on a presence or absence of, or on property of at least one such fragment, the methylation state of at least one CpG dinucleotide sequence of one or more sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences thereof. Preferably, the digested or undigested genomic DNA is amplified prior to said determining.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table

5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Additional aspects of the invention provide novel genomic and modified nucleic acid sequences, as well as oligonucleotides and/or PNA-oligomers for analysis of cytosine methylation patterns within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1 to 3 are ranked matrices produced from bisulfite sequencing data. The overall matrix represents the sequencing data for one fragment. Each row of the matrix represents a single CpG site within the fragment and each column represents an individual sample. The bar on the left represents a scale of the percent of methylation, with the degree of methylation represented by the shade of each position within the column from black representing 100% methylation to light grey representing 0% methylation. No data was available for white positions.

Figure 1 shows the sequencing data of a fragment of the gene Prostaglandin E2 Receptor, EP4 Subtype wherein the sequenced samples are from prostate carcinoma.

Figure 2 shows the sequencing data of a fragment of the gene Orphan Nuclear Receptor (a-1Fetoprotein Transcription Factor wherein the sequenced samples are from prostate carcinoma.

Figure 3 shows the sequencing data of a fragment of the gene 1-Acyl-SN-Glycerol-3-Phosphate Acyltransferase Gamma wherein the sequenced samples are from prostate carcinoma.

Figure 4 shows Normal prostate and BPH vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set.

The right plot gives accuracy, sensitivity and specificity of a linear SVM trained on methylation measurements from all oligonucleotides. The accuracy of each genomic region is represented as black squares, the specificity as unfilled diamonds, the sensitivity as unfilled squares. The accuracy as measured on the X-axis shows the fraction of correctly classified samples.

Figure 5 shows the best 12 markers for Normal prostate and BPH vs. Prostate Cancer differentiation according to Example 3. Normal prostate and BPH samples are shown on the left. Prostate cancer is on the right. Each column represents one sample; each row one oligonucleotide. Oligonucleotides are grouped by candidate marker. The indicated markers are ordered from top to bottom with increasing accuracy. On the right side of each marker, Bonferroni corrected p-values are listed. Methylation data are centered and normalized to one standard deviation for individual oligonucleotides. The color represents the relative distance of the oligonucleotide methylation status from the mean value. Green color represents hypomethylated CpGs within an oligonucleotide while red indicates hypermethylated CpGs within an oligonucleotide.

Figure 6 shows Normal Prostate, BPH and Other Tissues vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set. The right plot shows accuracy, sensitivity and specificity of a linear SVM trained on methylation measurements from all oligonucleotides. The accuracy of each genomic region is represented as black squares, the specificity as unfilled diamonds, the sensitivity as unfilled squares. The accuracy as measured on the X-axis shows the fraction of correctly classified samples.

Figure 7 shows the best 12 markers for Normal Prostate, BPH and Other Tissues vs. Prostate Cancer differentiation according to Example 3. Normal Prostate, BPH and Other Tissues samples are shown on the left. The 'Other Tissues' included normal tissue from other organs and cancer of other origins than prostate, according to table 7. Prostate cancer is on the right. Each column represents one sample; each row one oligonucleotide. Oligonucleotides are grouped by candidate marker. The indicated markers are ordered from top to bottom with increasing accuracy. On the right side of each marker, Bonferroni corrected p-values are listed. Methylation data are centered and normalized to one standard deviation for individual oligonucleotides. The color represents the relative distance of the oligonucleotide methylation

status from the mean value. Green color represents hypomethylated CpGs within an oligonucleotide while red indicates hypermethylated CpGs within an oligonucleotide.

Figure 8 shows Normal Prostate, BPH and Other Tissues vs. Prostate Cancer marker rankings according to Example 3. Each individual genomic region of interest is represented as a point. The left plot gives uncorrected p-values from the genewise logistic regression model. Lower and upper dotted lines show 5% Bonferroni and FDR limits respectively. The X-axis shows the p values for the individual CpG positions. The p values are the probabilities that the observed distribution occurred by chance in the data set. The following cancers are shown from left to right: bladder, melanoma, testes, kidney, endometrial cancer, lung, breast, pancreatic, liver, ovarian, salivary gland, and prostate.

DETAILED DESCRIPTION OF THE INVENTION

Definitions:

The term “CpG island” refers to a contiguous region of genomic DNA that satisfies the criteria of (1) having a frequency of CpG dinucleotides corresponding to an “Observed/Expected Ratio” >0.6 , and (2) having a “GC Content” >0.5 . CpG islands are typically, but not always, between about 0.2 to about 1 kb in length.

The term “methylation state” or “methylation status” refers to the presence or absence of 5-methylcytosine (“5-mCyt”) at one or a plurality of CpG dinucleotides within a DNA sequence. Methylation states at one or more particular palindromic CpG methylation sites (each having two CpG CpG dinucleotide sequences) within a DNA sequence include “unmethylated,” “fully-methylated” and “hemi-methylated.”

The term “hypermethylation” refers to the average methylation state corresponding to an *increased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term “hypomethylation” refers to the average methylation state corresponding to a *decreased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term "microarray" refers broadly to both "DNA microarrays," and 'DNA chip(s),' as recognized in the art, encompasses all art-recognized solid supports, and encompasses all methods for affixing nucleic acid molecules thereto or synthesis of nucleic acids thereon.

"Genetic parameters" are mutations and polymorphisms of genes and sequences further required for their regulation. To be designated as mutations are, in particular, insertions, deletions, point mutations, inversions and polymorphisms and, particularly preferred, SNPs (single nucleotide polymorphisms).

"Epigenetic parameters" are, in particular, cytosine methylations. Further epigenetic parameters include, for example, the acetylation of histones which, however, cannot be directly analyzed using the described method but which, in turn, correlate with the DNA methylation.

The term "bisulfite reagent" refers to a reagent comprising bisulfite, disulfite, hydrogen sulfite or combinations thereof, useful as disclosed herein to distinguish between methylated and unmethylated CpG dinucleotide sequences.

The term "Methylation assay" refers to any assay for determining the methylation state of one or more CpG dinucleotide sequences within a sequence of DNA.

The term "MS.AP-PCR" (Methylation-Sensitive Arbitrarily-Primed Polymerase Chain Reaction) refers to the art-recognized technology that allows for a global scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG dinucleotides, and described by Gonzalgo et al., *Cancer Research* 57:594-599, 1997.

The term "MethyLight™" refers to the art-recognized fluorescence-based real-time PCR technique described by Eads et al., *Cancer Res.* 59:2302-2306, 1999.

The term "HeavyMethyl™" assay, in the embodiment thereof implemented herein, refers to a HeavyMethyl™ refer to the use of methylation specific *blocking* probes covering CpG positions between the amplification primers.

The term "Ms-SNuPE" (Methylation-sensitive Single Nucleotide Primer Extension) refers to the art-recognized assay described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

The term "MSP" (Methylation-specific PCR) refers to the art-recognized methylation assay described by Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996, and by US Patent No. 5,786,146.

The term "COBRA" (Combined Bisulfite Restriction Analysis) refers to the art-recognized methylation assay described by Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997.

The term "MCA" (Methylated CpG Island Amplification) refers to the methylation assay described by Toyota et al., *Cancer Res.* 59:2307-12, 1999, and in WO 00/26401A1.

The term "hybridization" is to be understood as a bond of an oligonucleotide to a complementary sequence along the lines of the Watson-Crick base pairings in the sample DNA, forming a duplex structure.

"Stringent hybridization conditions," as defined herein, involve hybridizing at 68°C in 5x SSC/5x Denhardt's solution/1.0% SDS, and washing in 0.2x SSC/0.1% SDS at room temperature, or involve the art-recognized equivalent thereof (e.g., conditions in which a hybridization is carried out at 60°C in 2.5 x SSC buffer, followed by several washing steps at 37°C in a low buffer concentration, and remains stable). Moderately stringent conditions, as defined herein, involve including washing in 3x SSC at 42°C, or the art-recognized equivalent thereof. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Guidance regarding such conditions is available in the art, for example, by Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, N.Y.; and Ausubel et al. (eds.), 1995, *Current Protocols in Molecular Biology*, (John Wiley & Sons, N.Y.) at Unit 2.10.

Overview:

The present invention provides for molecular genetic markers that have novel utility for the analysis of methylation patterns associated with the development of prostate cell proliferative disorders. Said markers may be used for detecting and/or distinguishing between prostate cell proliferative disorders, thereby providing improved means for the classification and treatment of said disorders. It is particularly preferred that the markers according to the invention be used as the basis for a diagnostic test to be used for prostate cancer, to be used as an alternative or adjunct test to current tests. In one embodiment of the method, such a diagnostic test may be used post PSA screening of individuals with elevated PSA levels.

Bisulfite modification of DNA is an art-recognized tool used to assess CpG methylation status. 5-methylcytosine is the most frequent covalent base modification in the DNA of eukaryotic cells. It plays a role, for example, in the regulation of the transcription, in genetic imprinting, and in tumorigenesis. Therefore, the identification of 5-methylcytosine as a component of genetic information is of considerable interest. However, 5-methylcytosine positions cannot be identified by sequencing, because 5-methylcytosine has the same base

pairing behavior as cytosine. Moreover, the epigenetic information carried by 5-methylcytosine is completely lost during, *e.g.*, PCR amplification.

The most frequently used method for analyzing DNA for the presence of 5-methylcytosine is based upon the specific reaction of bisulfite with cytosine whereby, upon subsequent alkaline hydrolysis, cytosine is converted to uracil which corresponds to thymine in its base pairing behavior. Significantly, however, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is *converted* in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridization behavior, can now be detected as the only remaining cytosine using standard, art-recognized molecular biological techniques, for example, by amplification and hybridization, or by sequencing. All of these techniques are based on differential base pairing properties, which can now be fully exploited.

The prior art, in terms of sensitivity, is defined by a method comprising enclosing the DNA to be analyzed in an agarose matrix, thereby preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and replacing all precipitation and purification steps with fast dialysis (Olek A, et al., A modified and improved method for bisulfite based cytosine methylation analysis, *Nucleic Acids Res.* 24:5064-6, 1996). It is thus possible to analyze individual cells for methylation status, illustrating the utility and sensitivity of the method. An overview of art-recognized methods for detecting 5-methylcytosine is provided by Rein, T., et al., *Nucleic Acids Res.*, 26:2255, 1998.

The bisulfite technique, barring few exceptions (*e.g.*, Zeschnigk M, et al., *Eur J Hum Genet.* 5:94-98, 1997), is currently only used in research. In all instances, short, specific fragments of a known gene are amplified subsequent to a bisulfite treatment, and either completely sequenced (Olek & Walter, *Nat Genet.* 1997 17:275-6, 1997), subjected to one or more primer extension reactions (Gonzalzo & Jones, *Nucleic Acids Res.*, 25:2529-31, 1997; WO 95/00669; U.S. Patent No. 6,251,594) to analyze individual cytosine positions, or treated by enzymatic digestion (Xiong & Laird, *Nucleic Acids Res.*, 25:2532-4, 1997). Detection by hybridization has also been described in the art (Olek et al., WO 99/28498). Additionally, use of the bisulfite technique for methylation detection with respect to individual genes has been described (Grigg & Clark, *Bioessays*, 16:431-6, 1994; Zeschnigk M, et al., *Hum Mol Genet.*, 6:387-95, 1997; Feil R, et al., *Nucleic Acids Res.*, 22:695-, 1994; Martin V, et al., *Gene*, 157:261-4, 1995; WO 9746705 and WO 9515373).

The present invention provides for the use of the bisulfite technique, in combination with one or more methylation assays, for determination of the methylation status of CpG

dinucleotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 . According to the present invention, determination of the methylation status of CpG dinucleotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 has diagnostic and prognostic utility.

Methylation Assay Procedures. Various methylation assay procedures are known in the art, and can be used in conjunction with the present invention. These assays allow for determination of the methylation state of one or a plurality of CpG dinucleotides (*e.g.*, CpG islands) within a DNA sequence. Such assays involve, among other techniques, DNA sequencing of bisulfite-treated DNA, PCR (for sequence-specific amplification), Southern blot analysis, and use of methylation-sensitive restriction enzymes.

For example, genomic sequencing has been simplified for analysis of DNA methylation patterns and 5-methylcytosine distribution by using bisulfite treatment (Frommer et al., *Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). Additionally, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used, *e.g.*, the method described by Sadri & Hornsby (*Nucl. Acids Res.* 24:5058-5059, 1996), or COBRA (Combined Bisulfite Restriction Analysis) (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997).

COBRA. COBRA analysis is a quantitative methylation assay useful for determining DNA methylation levels at specific gene loci in small amounts of genomic DNA (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997). Briefly, restriction enzyme digestion is used to reveal methylation-dependent sequence differences in PCR products of sodium bisulfite-treated DNA. Methylation-dependent sequence differences are first introduced into the genomic DNA by standard bisulfite treatment according to the procedure described by Frommer et al. (*Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). PCR amplification of the bisulfite converted DNA is then performed using primers specific for the interested CpG islands, followed by restriction endonuclease digestion, gel electrophoresis, and detection using specific, labeled hybridization probes. Methylation levels in the original DNA sample are represented by the relative amounts of digested and undigested PCR product in a linearly quantitative fashion across a wide spectrum of DNA methylation levels. In addition, this technique can be reliably applied to DNA obtained from microdissected paraffin-embedded tissue samples. Typical reagents (*e.g.*, as might be found in a typical COBRA-based kit) for COBRA analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridization oligo; control hybridization oligo; kinase labeling kit for oligo probe; and

radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kits (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

Preferably, assays such as "MethyLight™" (a fluorescence-based real-time PCR technique) (Eads et al., *Cancer Res.* 59:2302-2306, 1999), Ms-SNuPE (Methylation-sensitive Single Nucleotide Primer Extension) reactions (Gonzalzo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997), methylation-specific PCR ("MSP"; Herman et al., *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146), and methylated CpG island amplification ("MCA"; Toyota et al., *Cancer Res.* 59:2307-12, 1999) are used alone or in combination with other of these methods.

MethyLight™. The MethyLight™ assay is a high-throughput quantitative methylation assay that utilizes fluorescence-based real-time PCR (TaqMan®) technology that requires no further manipulations after the PCR step (Eads et al., *Cancer Res.* 59:2302-2306, 1999). Briefly, the MethyLight™ process begins with a mixed sample of genomic DNA that is converted, in a sodium bisulfite reaction, to a mixed pool of methylation-dependent sequence differences according to standard procedures (the bisulfite process converts unmethylated cytosine residues to uracil). Fluorescence-based PCR is then performed either in an "unbiased" (with primers that do not overlap known CpG methylation sites) PCR reaction, or in a "biased" (with PCR primers that overlap known CpG dinucleotides) reaction. Sequence discrimination can occur either at the level of the amplification process or at the level of the fluorescence detection process, or both.

The MethyLight™ assay may be used as a quantitative test for methylation patterns in the genomic DNA sample, wherein sequence discrimination occurs at the level of probe hybridization. In this quantitative version, the PCR reaction provides for unbiased amplification in the presence of a fluorescent probe that overlaps a particular putative methylation site. An unbiased control for the amount of input DNA is provided by a reaction in which neither the primers, nor the probe overlap any CpG dinucleotides. Alternatively, a qualitative test for genomic methylation is achieved by probing of the biased PCR pool with either control oligonucleotides that do not "cover" known methylation sites (a fluorescence-based version of the "MSP" technique), or with oligonucleotides covering potential methylation sites.

The MethyLight™ process can be used with a "TaqMan®" probe in the amplification process. For example, double-stranded genomic DNA is treated with sodium bisulfite and subjected to one of two sets of PCR reactions using TaqMan® probes; e.g., with either biased

primers and TaqMan® probe, or unbiased primers and TaqMan® probe. The TaqMan® probe is dual-labeled with fluorescent “reporter” and “quencher” molecules, and is designed to be specific for a relatively high GC content region so that it melts out at about 10°C higher temperature in the PCR cycle than the forward or reverse primers. This allows the TaqMan® probe to remain fully hybridized during the PCR annealing/extension step. As the Taq polymerase enzymatically synthesizes a new strand during PCR, it will eventually reach the annealed TaqMan® probe. The Taq polymerase 5' to 3' endonuclease activity will then displace the TaqMan® probe by digesting it to release the fluorescent reporter molecule for quantitative detection of its now unquenched signal using a real-time fluorescent detection system.

Typical reagents (*e.g.*, as might be found in a typical MethyLight™-based kit) for MethyLight™ analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); TaqMan® probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

Ms-SNuPE. The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalzo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997). Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired target sequence is then performed using PCR primers specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest. Small amounts of DNA can be analyzed (*e.g.*, microdissected pathology sections), and it avoids utilization of restriction enzymes for determining the methylation status at CpG sites.

Typical reagents (*e.g.*, as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer (for the Ms-SNuPE reaction); and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kit (*e.g.*, precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

MSP. MSP (methylation-specific PCR) allows for assessing the methylation status of virtually any group of CpG sites within a CpG island, independent of the use of methylation-

sensitive restriction enzymes (Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146). Briefly, DNA is modified by sodium bisulfite which converts all unmethylated, but not methylated cytosines to uracil. DNA can subsequently be amplified with primers specific for methylated versus unmethylated DNA. MSP requires only small quantities of DNA, is sensitive to 0.1% methylated alleles of a given CpG island locus, and can be performed on DNA extracted from paraffin-embedded samples. Typical reagents (*e.g.*, as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes.

MCA. The MCA technique is a method that can be used to screen for altered methylation patterns in genomic DNA, and to isolate specific sequences associated with these changes (Toyota et al., *Cancer Res.* 59:2307-12, 1999). Briefly, restriction enzymes with different sensitivities to cytosine methylation in their recognition sites are used to digest genomic DNAs from primary tumors, cell lines, and normal tissues prior to arbitrarily primed PCR amplification. Fragments that show differential methylation are cloned and sequenced after resolving the PCR products on high-resolution polyacrylamide gels. The cloned fragments are then used as probes for Southern analysis to confirm differential methylation of these regions. Typical reagents (*e.g.*, as might be found in a typical MCA-based kit) for MCA analysis may include, but are not limited to: PCR primers for arbitrary priming Genomic DNA; PCR buffers and nucleotides, restriction enzymes and appropriate buffers; gene-hybridization oligos or probes; control hybridization oligos or probes.

HeavyMethyl. The HeavyMethyl technique is a means for selectively amplifying methylated as opposed to non-methylated DNA (or vice versa). Blocker oligonucleotides specific to either methylated or unmethylated versions of a bisulfite treated target sequence are hybridised to the treated nucleic acids. The sample is then enzymatically amplified, wherein the hybridisation of the blocker oligonucleotides hinders amplification of the nucleic acid strand to which it is bound. Typical reagents (*e.g.*, as might be found in a typical HeavyMethyl-based kit) for HeavyMethyl analysis may include, but are not limited to: methylated or unmethylated blocker oligonucleotides for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes and primers.

GENOMIC SEQUENCES ACCORDING TO SEQ ID NO: 1 to SEQ ID NO: 59 , AND TREATED VARIANTS THEREOF ACCORDING TO SEQ ID NO: 60 to SEQ ID NO: 295, WERE DETERMINED TO HAVE UTILITY FOR THE DETECTION AND/OR CLASSIFICATION OF PROSTATE CELL PROLIFERATIVE DISORDERS.

The present invention is based upon the analysis of methylation levels within one or more genomic sequences taken from the group consisting SEQ ID NO: 1 to SEQ ID NO: 59 .

Particular embodiments of the present invention provide a novel application of the analysis of methylation levels and/or patterns within said sequences that enables a precise detection and/or classification of prostate cell proliferative disorders. Early detection of prostate cell proliferative disorders is directly linked with disease prognosis, and the disclosed method thereby enables the physician and patient to make better and more informed treatment decisions.

FURTHER IMPROVEMENTS

The present invention provides novel uses for genomic sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 . Additional embodiments provide modified variants of SEQ ID NO: 1 to SEQ ID NO: 59 , as well as oligonucleotides and/or PNA-oligomers for analysis of cytosine methylation patterns within SEQ ID NO: 1 to SEQ ID NO: 59 .

An objective of the invention comprises analysis of the methylation state of one or more CpG dinucleotides within at least one of the genomic sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 59 and sequences complementary thereto.

The disclosed invention provides treated nucleic acids, derived from genomic SEQ ID NO: 1 to SEQ ID NO 59, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization. The genomic sequences in question may comprise one, or more, consecutive or random methylated CpG positions. Said treatment preferably comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof. In a preferred embodiment of the invention, the objective comprises analysis of a modified nucleic acid comprising a sequence of at least 16 contiguous nucleotide bases in length of a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and preferably wherein said sequence comprises at least one CpG, TpA or CpA dinucleotide and sequences complementary thereto. The sequences of SEQ ID NO: 60 to SEQ ID NO: 295 provide modified versions of the

nucleic acid according to SEQ ID NO: 1 to SEQ ID NO: 59 , wherein the modification of each genomic sequence results in the synthesis of a nucleic acid having a sequence that is unique and distinct from said genomic sequence as follows. For each sense strand genomic DNA, e.g., SEQ ID NO:1, four converted versions are disclosed. A first version wherein "C" → "T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for the genomic sequence, all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted). For each genomic sequence SEQ ID NO:1 to SEQ ID NO:59) the equivalent sequence can be identified as SEQ ID NO. = 60 + (X-1)2, wherein X = SEQ ID NO. of the genomic sequence. Therefore, the pretreated equivalent sequence to SEQ ID NO:1 is SEQ ID NO:60, the equivalent sequence to SEQ ID NO:2 is SEQ ID NO: 62 and the equivalent sequence to SEQ ID NO:3 is SEQ ID NO: 64. A second version discloses the complement of the disclosed genomic DNA sequence (*i.e.* *antisense* strand), wherein "C" → "T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted). For each genomic sequence SEQ ID NO:1 to SEQ ID NO:59) the equivalent sequence can be identified as SEQ ID NO. = 61 + (X-1)2, wherein X = SEQ ID NO. of the genomic sequence. Therefore, the pretreated equivalent sequence to SEQ ID NO:1 is SEQ ID NO:61, the equivalent sequence to SEQ ID NO:2 is SEQ ID NO: 63 and the equivalent sequence to SEQ ID NO:3 is SEQ ID NO: 65. The 'upmethylated' converted sequences of SEQ ID NO: 1 to SEQ ID NO: 59 correspond to SEQ ID NO: 60 to SEQ ID NO: 177. A third chemically converted version of each genomic sequences is provided, wherein "C" → "T" for all "C" residues, including those of "CpG" dinucleotide sequences (*i.e.*, corresponds to case where, for the genomic sequences, all "C" residues of CpG dinucleotide sequences are unmethylated). For each genomic sequence SEQ ID NO:1 to SEQ ID NO:59) the equivalent sequence can be identified as SEQ ID NO. = 178 + (X-1)2, wherein X = SEQ ID NO. of the genomic sequence. Therefore, the pretreated equivalent sequence to SEQ ID NO:1 is SEQ ID NO:178, the equivalent sequence to SEQ ID NO:2 is SEQ ID NO: 180 and the equivalent sequence to SEQ ID NO:3 is SEQ ID NO: 182. A final chemically converted version of each sequence, discloses the complement of the disclosed genomic DNA sequence (*i.e.* *antisense* strand), wherein "C" → "T" for all "C" residues, including those of "CpG" dinucleotide sequences (*i.e.*, corresponds to case where, for the complement (*antisense* strand) of each genomic sequence, all "C" residues of CpG dinucleotide sequences are unmethylated). For each genomic sequence SEQ ID NO:1 to SEQ ID NO:59) the equivalent sequence can be identified as SEQ ID NO. = 179 + (X-1)2, wherein X = SEQ ID NO. of the genomic sequence. Therefore, the pretreated equivalent sequence to

SEQ ID NO:1 is SEQ ID NO:179, the equivalent sequence to SEQ ID NO:2 is SEQ ID NO: 181 and the equivalent sequence to SEQ ID NO:3 is SEQ ID NO: 183. The 'downmethylated' converted sequences of SEQ ID NO: 1 to SEQ ID NO: 59 correspond to SEQ ID NO: 177 to SEQ ID NO: 295. Further descriptions of the genomic sequences are in Table 8, including, in some cases, gene names. In some cases, the sequences are not within coding regions of genes and gene names have therefore not been given.

In an alternative preferred embodiment, such analysis comprises the use of an oligonucleotide or oligomer for detecting the cytosine methylation state within genomic or pretreated (chemically modified) DNA, according to SEQ ID NO: 1 to SEQ ID NO: 295. Said oligonucleotide or oligomer comprising a nucleic acid sequence having a length of at least nine (9) nucleotides which hybridizes, under moderately stringent or stringent conditions (as defined herein above), to a pretreated nucleic acid sequence according to SEQ ID NO: 60 to SEQ ID NO: 295 and/or sequences complementary thereto, or to a genomic sequence according to SEQ ID NO: 1 to SEQ ID NO: 59 and/or sequences complementary thereto.

Thus, the present invention includes nucleic acid molecules (*e.g.*, oligonucleotides and peptide nucleic acid (PNA) molecules (PNA-oligomers)) that hybridize under moderately stringent and/or stringent hybridization conditions to all or a portion of the sequences SEQ ID NO: 1 to SEQ ID NO: 295, or to the complements thereof. The hybridizing portion of the hybridizing nucleic acids is typically at least 9, 15, 20, 25, 30 or 35 nucleotides in length. However, longer molecules have inventive utility, and are thus within the scope of the present invention.

Preferably, the hybridizing portion of the inventive hybridizing nucleic acids is at least 95%, or at least 98%, or 100% identical to the sequence, or to a portion thereof of SEQ ID NO: 1 to SEQ ID NO: 295, or to the complements thereof.

Hybridizing nucleic acids of the type described herein can be used, for example, as a primer (*e.g.*, a PCR primer), or a diagnostic and/or prognostic probe or primer. Preferably, hybridization of the oligonucleotide probe to a nucleic acid sample is performed under stringent conditions and the probe is 100% identical to the target sequence. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or T_m , which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required stringency conditions.

For target sequences that are related and substantially identical to the corresponding sequence of SEQ ID NO: 1 to SEQ ID NO: 59 (such as allelic variants and SNPs), rather than

identical, it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (*e.g.*, SSC or SSPE). Then, assuming that 1% mismatching results in a 1°C decrease in the T_m , the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequences having > 95% identity with the probe are sought, the final wash temperature is decreased by 5°C). In practice, the change in T_m can be between 0.5°C and 1.5°C per 1% mismatch.

Examples of inventive oligonucleotides of length X (in nucleotides), as indicated by polynucleotide positions with reference to, *e.g.*, SEQ ID NO:1, include those corresponding to sets (sense and antisense sets) of consecutively overlapping oligonucleotides of length X , where the oligonucleotides within each consecutively overlapping set (corresponding to a given X value) are defined as the finite set of Z oligonucleotides from nucleotide positions:

n to $(n + (X-1))$;

where $n=1, 2, 3, \dots, (Y-(X-1))$;

where Y equals 2299 base pairs.

where X equals the common length (in nucleotides) of each oligonucleotide in the set (*e.g.*, $X=20$ for a set of consecutively overlapping 20-mers); and

where the number (Z) of consecutively overlapping oligomers of length X for a given SEQ ID NO of length Y is equal to $Y-(X-1)$.

Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

Examples of inventive 20-mer oligonucleotides include the following set of 2299 oligomers (and the antisense set complementary thereto), indicated by polynucleotide positions with reference to SEQ ID NO:1 1-20, 2-21, 3-22, 4-23, 5-24,

Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

The present invention encompasses, for *each* of SEQ ID NO: 1 to SEQ ID NO: 295 (sense and antisense), multiple consecutively overlapping sets of oligonucleotides or modified oligonucleotides of length X , where, *e.g.*, $X= 9, 10, 17, 20, 22, 23, 25, 27, 30$ or 35 nucleotides.

The oligonucleotides or oligomers according to the present invention constitute effective tools useful to ascertain genetic and epigenetic parameters of the genomic sequence corresponding to SEQ ID NO: 1 to SEQ ID NO: 59 . Preferred sets of such oligonucleotides or modified oligonucleotides of length X are those consecutively overlapping sets of

oligomers corresponding to SEQ ID NO: 1 to SEQ ID NO: 295 (and to the complements thereof). Preferably, said oligomers comprise at least one CpG, TpG or CpA dinucleotide.

Particularly preferred oligonucleotides or oligomers according to the present invention are those in which the cytosine of the CpG dinucleotide (or of the corresponding converted TpG or CpA dinucleotide) sequences is within the middle third of the oligonucleotide; that is, where the oligonucleotide is, for example, 13 bases in length, the CpG, TpG or CpA dinucleotide is positioned within the fifth to ninth nucleotide from the 5'-end.

The oligonucleotides of the invention can also be modified by chemically linking the oligonucleotide to one or more moieties or conjugates to enhance the activity, stability or detection of the oligonucleotide. Such moieties or conjugates include chromophores, fluorophors, lipids such as cholesterol, cholic acid, thioether, aliphatic chains, phospholipids, polyamines, polyethylene glycol (PEG), palmityl moieties, and others as disclosed in, for example, United States Patent Numbers 5,514,758, 5,565,552, 5,567,810, 5,574,142, 5,585,481, 5,587,371, 5,597,696 and 5,958,773. The probes may also exist in the form of a PNA (peptide nucleic acid) which has particularly preferred pairing properties. Thus, the oligonucleotide may include other appended groups such as peptides, and may include hybridization-triggered cleavage agents (Krol et al., *BioTechniques* 6:958-976, 1988) or intercalating agents (Zon, *Pharm. Res.* 5:539-549, 1988). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a chromophore, fluorophor, peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The oligonucleotide may also comprise at least one art-recognized modified sugar and/or base moiety, or may comprise a modified backbone or non-natural internucleoside linkage.

The oligonucleotides or oligomers according to particular embodiments of the present invention are typically used in 'sets,' which contain at least one oligomer for analysis of each of the CpG dinucleotides of genomic sequence SEQ ID NO: 1 to SEQ ID NO: 59 and sequences complementary thereto, or to the corresponding CpG, TpG or CpA dinucleotide within a sequence of the pretreated nucleic acids according to SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto. However, it is anticipated that for economic or other factors it may be preferable to analyze a limited selection of the CpG dinucleotides within said sequences, and the content of the set of oligonucleotides is altered accordingly.

Therefore, in particular embodiments, the present invention provides a set of at least two (2) (oligonucleotides and/or PNA-oligomers) useful for detecting the cytosine

methylation state in pretreated genomic DNA (SEQ ID NO: 60 to SEQ ID NO: 295), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 59 and sequences complementary thereto). These probes enable detection and/or classification of genetic and epigenetic parameters of prostate cell proliferative disorders. The set of oligomers may also be used for detecting single nucleotide polymorphisms (SNPs) in pretreated genomic DNA (SEQ ID NO: 60 to SEQ ID NO: 295), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 59 and sequences complementary thereto).

In preferred embodiments, at least one, and more preferably all members of a set of oligonucleotides is bound to a solid phase.

In further embodiments, the present invention provides a set of at least two (2) oligonucleotides that are used as 'primer' oligonucleotides for amplifying DNA sequences of one of SEQ ID NO: 1 to SEQ ID NO: 295 and sequences complementary thereto, or segments thereof.

It is anticipated that the oligonucleotides may constitute all or part of an "array" or "DNA chip" (*i.e.*, an arrangement of different oligonucleotides and/or PNA-oligomers bound to a solid phase). Such an array of different oligonucleotide- and/or PNA-oligomer sequences can be characterized, for example, in that it is arranged on the solid phase in the form of a rectangular or hexagonal lattice. The solid-phase surface may be composed of silicon, glass, polystyrene, aluminum, steel, iron, copper, nickel, silver, or gold. Nitrocellulose as well as plastics such as nylon, which can exist in the form of pellets or also as resin matrices, may also be used. An overview of the Prior Art in oligomer array manufacturing can be gathered from a special edition of Nature Genetics (*Nature Genetics Supplement*, Volume 21, January 1999, and from the literature cited therein). Fluorescently labeled probes are often used for the scanning of immobilized DNA arrays. The simple attachment of Cy3 and Cy5 dyes to the 5'-OH of the specific probe are particularly suitable for fluorescence labels. The detection of the fluorescence of the hybridized probes may be carried out, for example, via a confocal microscope. Cy3 and Cy5 dyes, besides many others, are commercially available.

It is particularly preferred that the oligomers according to the invention are utilised for at least one of: detection of; detection and differentiation between or among subclasses of; diagnosis of; prognosis of; treatment of; monitoring of; and treatment and monitoring of prostate cell proliferative disorders. This is enabled by use of said sets for the detection or detection and differentiation of prostate cell proliferative disorders.

The present invention further provides a method for ascertaining genetic and/or epigenetic parameters of the genomic sequences according to SEQ ID NO: 1 to SEQ ID NO:

59 within a subject by analyzing cytosine methylation and single nucleotide polymorphisms. Said method comprising contacting a nucleic acid comprising one or more of SEQ ID NO: 1 to SEQ ID NO: 59 in a biological sample obtained from said subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said nucleotide sequence(s) comprise, or hybridizes to, one or more more sequences comprising at least 16 contiguous nucleotides of the sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Preferably, said method comprises the following steps: In the *first step*, a sample of the tissue to be analysed is obtained. The source may be any suitable source, such as cell lines, histological slides, biopsies, tissue embedded in paraffin, bodily fluids, ejaculate, urine, blood and all possible combinations thereof. In a particularly preferred embodiment of the method said source is bodily fluids including post prostatic massage urine, ejaculate, urine, or blood. The DNA is then isolated from the sample. Extraction may be by means that are standard to one skilled in the art, including the use of commercially available kits, detergent lysates, sonification and vortexing with glass beads. Briefly, wherein the DNA of interest is encapsulated by a cellular membrane the biological sample must be disrupted and lysed by enzymatic, chemical or mechanical means. The DNA solution may then be cleared of proteins and other contaminants e.g. by digestion with proteinase K. The genomic DNA is then recovered from the solution. This may be carried out by means of a variety of methods including salting out, organic extraction or binding of the DNA to a solid phase support. The

choice of method will be affected by several factors including time, expense and required quantity of DNA.

Once the nucleic acids have been extracted, the genomic double stranded DNA is used in the analysis.

In the *second step* of the method, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridization behavior. This will be understood as 'pretreatment' herein.

The above-described treatment of genomic DNA is preferably carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis that results in a conversion of non-methylated cytosine nucleobases to uracil or to another base that is dissimilar to cytosine in terms of base pairing behavior.

In the *third step* of the method, fragments of the pretreated DNA are amplified, using sets of primer oligonucleotides according to the present invention, and an amplification enzyme. The amplification of several DNA segments can be carried out simultaneously in one and the same reaction vessel. Typically, the amplification is carried out using a polymerase chain reaction (PCR). The set of primer oligonucleotides includes at least two oligonucleotides whose sequences are each reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base sequences of one or more of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto.

In an alternate embodiment of the method, the methylation status of preselected CpG positions within the nucleic acid sequences comprising one or more of SEQ ID NO: 1 to SEQ ID NO: 59 may be detected by use of methylation-specific primer oligonucleotides. This technique (MSP) has been described in United States Patent No. 6,265,171 to Herman. The use of methylation status specific primers for the amplification of bisulfite treated DNA allows the differentiation between methylated and unmethylated nucleic acids. MSP primers pairs contain at least one primer that hybridizes to a bisulfite treated CpG dinucleotide. Therefore, the sequence of said primers comprises at least one CpG dinucleotide. MSP primers specific for non-methylated DNA contain a "T" at the 3' position of the C position in the CpG. Preferably, therefore, the base sequence of said primers is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences

complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretetreated sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretetreated sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretetreated sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

A further preferred embodiment of the method comprises the use of *blocker* oligonucleotides. The use of such blocker oligonucleotides has been described by Yu et al., *BioTechniques* 23:714-720, 1997. Blocking probe oligonucleotides are hybridized to the bisulfite treated nucleic acid concurrently with the PCR primers. PCR amplification of the nucleic acid is terminated at the 5' position of the blocking probe, such that amplification of a nucleic acid is suppressed where the complementary sequence to the blocking probe is present. The probes may be designed to hybridize to the bisulfite treated nucleic acid in a methylation status specific manner. For example, for detection of methylated nucleic acids within a population of unmethylated nucleic acids, suppression of the amplification of nucleic acids which are unmethylated at the position in question would be carried out by the use of blocking probes comprising a 'CpA' or 'TpA' at the position in question, as opposed to a 'CpG' if the suppression of amplification of methylated nucleic acids is desired.

For PCR methods using blocker oligonucleotides, efficient disruption of polymerase-mediated amplification requires that blocker oligonucleotides not be elongated by the polymerase. Preferably, this is achieved through the use of blockers that are 3'-deoxyoligonucleotides, or oligonucleotides derivitized at the 3' position with other than a "free" hydroxyl group. For example, 3'-O-acetyl oligonucleotides are representative of a preferred class of blocker molecule.

Additionally, polymerase-mediated decomposition of the blocker oligonucleotides should be precluded. Preferably, such preclusion comprises either use of a polymerase lacking 5'-3' exonuclease activity, or use of modified blocker oligonucleotides having, for example, thioate bridges at the 5'-termini thereof that render the blocker molecule nuclease-resistant. Particular applications may not require such 5' modifications of the blocker. For example, if the blocker- and primer-binding sites overlap, thereby precluding binding of the primer (*e.g.*, with excess blocker), degradation of the blocker oligonucleotide will be substantially precluded. This is because the polymerase will not extend the primer toward, and through (in the 5'-3' direction) the blocker—a process that normally results in degradation of the hybridized blocker oligonucleotide.

A particularly preferred blocker/PCR embodiment, for purposes of the present invention and as implemented herein, comprises the use of peptide nucleic acid (PNA) oligomers as blocking oligonucleotides. Such PNA blocker oligomers are ideally suited, because they are neither decomposed nor extended by the polymerase.

Preferably, therefore, the base sequence of said *blocking oligonucleotides* is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto, wherein the base sequence of said oligonucleotides comprises at least one CpG, TpG or CpA dinucleotide.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

The fragments obtained by means of the amplification can carry a directly or indirectly detectable label. Preferred are labels in the form of fluorescence labels, radionuclides, or detachable molecule fragments having a typical mass that can be detected in a mass spectrometer. Where said labels are mass labels, it is preferred that the labeled amplificates have a single positive or negative net charge, allowing for better detectability in the mass spectrometer. The detection may be carried out and visualized by means of, e.g., matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-TOF) is a very efficient development for the analysis of biomolecules (Karas & Hillenkamp, *Anal Chem.*, 60:2299-301, 1988). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapour phase in an unfragmented manner. The analyte is ionized by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones. MALDI-TOF spectrometry is well suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut & Beck, *Current Innovations and Future Trends*, 1:147-57, 1995). The sensitivity with respect to nucleic acid analysis is approximately 100-times less than for peptides, and decreases disproportionally with increasing fragment size. Moreover, for nucleic acids having a multiply negatively charged backbone, the ionization process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity between peptides and nucleic acids has not been reduced. This difference in sensitivity can be reduced, however, by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. For example, phosphorothioate nucleic acids, in which the usual phosphates of the backbone are substituted with thiophosphates, can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut & Beck, *Nucleic Acids Res.* 23: 1367-73, 1995). The coupling of a charge tag to this modified DNA results in an increase in MALDI-TOF sensitivity to the same level as that found for peptides. A further advantage of charge tagging is the increased stability of the analysis against impurities, which makes the detection of unmodified substrates considerably more difficult.

In the *fourth step* of the method, the amplicates obtained during the third step of the method are analysed in order to ascertain the methylation status of the CpG dinucleotides prior to the treatment.

In embodiments where the amplicates were obtained by means of MSP amplification, the presence or absence of an amplicate is in itself indicative of the methylation state of the CpG positions covered by the primer, according to the base sequences of said primer.

Amplicates obtained by means of both standard and methylation specific PCR may be further analyzed by means of hybridization-based methods such as, but not limited to, array technology and probe based technologies as well as by means of techniques such as sequencing and template directed extension.

In one embodiment of the method, the amplicates synthesised in *step three* are subsequently hybridized to an array or a set of oligonucleotides and/or PNA probes. In this context, the hybridization takes place in the following manner: the set of probes used during the hybridization is preferably composed of at least 2 oligonucleotides or PNA-oligomers; in the process, the amplicates serve as probes which hybridize to oligonucleotides previously bonded to a solid phase; the non-hybridized fragments are subsequently removed; said oligonucleotides contain at least one base sequence having a length of at least 9 nucleotides which is reverse complementary or identical to a segment of the base sequences specified in the present Sequence Listing; and the segment comprises at least one CpG , TpG or CpA dinucleotide.

In a preferred embodiment, said dinucleotide is present in the central third of the oligomer. For example, wherein the oligomer comprises one CpG dinucleotide, said dinucleotide is preferably the fifth to ninth nucleotide from the 5'-end of a 13-mer. One oligonucleotide exists for the analysis of each CpG dinucleotide within the sequence according to SEQ ID NO: 1 to SEQ ID NO: 59 , and the equivalent positions within SEQ ID NO: 60 to SEQ ID NO: 295. Said oligonucleotides may also be present in the form of peptide nucleic acids. The non-hybridized amplicates are then removed. The hybridized amplicates are then detected. In this context, it is preferred that labels attached to the amplicates are identifiable at each position of the solid phase at which an oligonucleotide sequence is located.

In yet a further embodiment of the method, the genomic methylation status of the CpG positions may be ascertained by means of oligonucleotide probes that are hybridised to the

bisulfite treated DNA concurrently with the PCR amplification primers (wherein said primers may either be methylation specific or standard).

A particularly preferred embodiment of this method is the use of fluorescence-based Real Time Quantitative PCR (Heid et al., *Genome Res.* 6:986-994, 1996; *also see* United States Patent No. 6,331,393) employing a dual-labeled fluorescent oligonucleotide probe (TaqMan™ PCR, using an ABI Prism 7700 Sequence Detection System, Perkin Elmer Applied Biosystems, Foster City, California). The TaqMan™ PCR reaction employs the use of a nonextendible interrogating oligonucleotide, called a TaqMan™ probe, which, in preferred imbodiments, is designed to hybridize to a GpC-rich sequence located between the forward and reverse amplification primers. The TaqMan™ probe further comprises a fluorescent "reporter moiety" and a "quencher moiety" covalently bound to linker moieties (*e.g.*, phosphoramidites) attached to the nucleotides of the TaqMan™ oligonucleotide. For analysis of methylation within nucleic acids subsequent to bisulfite treatment, it is required that the probe be methylation specific, as described in United States Patent No. 6,331,393, (hereby incorporated by reference in its entirety) also known as the MethylLight™ assay. Variations on the TaqMan™ detection methodology that are also suitable for use with the described invention include the use of dual-probe technology (Lightcycler™) or fluorescent amplification primers (Sunrise™ technology). Both these techniques may be adapted in a manner suitable for use with bisulfite treated DNA, and moreover for methylation analysis within CpG dinucleotides.

A further suitable method for the use of probe oligonucleotides for the assessment of methylation by analysis of bisulfite treated nucleic acids In a further preferred embodiment of the method, the *fifth step* of the method comprises the use of template-directed oligonucleotide extension, such as MS-SNuPE as described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

In yet a further embodiment of the method, the *fifth step* of the method comprises sequencing and subsequent sequence analysis of the amplificate generated in the *third step* of the method (Sanger F., et al., *Proc Natl Acad Sci USA* 74:5463-5467, 1977).

In one preferred embodiment of the method the nucleic acids according to SEQ ID NO: 1 to SEQ ID NO 59 are isolated and treated according to the first three steps of the method outlined above, namely:

- a. obtaining, from a subject, a biological sample having subject genomic DNA;

- b. extracting or otherwise isolating the genomic DNA;
- c. treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

and wherein the subsequent amplification of d) is carried out in a methylation specific manner, namely by use of methylation specific primers or *blocking oligonucleotides*, and further wherein the detection of the amplicates is carried out by means of a real-time detection probes, as described above.

Wherein the subsequent amplification of d) is carried out by means of methylation specific primers, as described above, said methylation specific primers comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said *blocking oligonucleotide* nucleotide sequence(s) hybridizes to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Step e) of the method, namely the detection of the specific amplicates indicative of the methylation status of one or more CpG positions according to SEQ ID NO: 1 to SEQ ID NO 59 is carried out by means of real-time detection methods as described above.

In an alternative most preferred embodiment of the method the subsequent amplification of d) is carried out in the presence of *blocking oligonucleotides*, as described above. Said *blocking oligonucleotides* comprising a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG, TpG or CpA dinucleotide. Step e) of the method, namely the detection of the specific amplicates indicative of the methylation status of one or more CpG positions according to SEQ ID NO: 1 to SEQ ID NO 59 is carried out by means of real-time detection methods as described above.

In a further preferred embodiment of the method the nucleic acids according to SEQ ID NO: 1 to SEQ ID NO 58 are isolated and treated according to the first three steps of the method outlined above, namely:

- a) obtaining, from a subject, a biological sample having subject genomic DNA;
- b) extracting or otherwise isolating the genomic DNA;
- c) treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties; and wherein

d) amplifying subsequent to treatment in c) is carried out in a methylation specific manner, namely by use of methylation specific primers or *blocking oligonucleotides*, and further wherein

e) detecting of the amplicates is carried out by means of a real-time detection probes, as described above.

Wherein the subsequent amplification of c) is carried out by means of methylation specific primers, as described above, said methylation specific primers comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 60 to SEQ ID NO: 295 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that said methylation specific primers

hybridize to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that said methylation specific primers hybridize to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that said methylation specific primers hybridize to a pretreated nucleic acid sequence according to one of the pretreated sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Additional embodiments of the invention provide a method for the analysis of the methylation status of genomic DNA according to the invention (SEQ ID NO: 1 to SEQ ID NO: 59 , and complements thereof) without the need for pretreatment.

Wherein the method is for the differentiation of one of normal prostate and/or BPH from prostate cancer it is particularly preferred that the analysis is carried out on genomic sequences according to Table 4, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of one of normal prostate, normal tissue from other tissues, cancer of other tissues and/or BPH from prostate cancer it is particularly preferred that the analysis is carried out on genomic sequences according to Table 5, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

Wherein the method is for the differentiation of prostate cancer from cancers of other tissues it is particularly preferred that the analysis is carried out on genomic sequences according to Table 6, said contiguous nucleotides comprising at least one CpG, TpG or CpA dinucleotide sequence.

In the *first step* of such additional embodiments, the genomic DNA sample is isolated from tissue or cellular sources. Preferably, such sources include cell lines, histological slides, body fluids, or tissue embedded in paraffin. In the *second step*, the genomic DNA is extracted. Extraction may be by means that are standard to one skilled in the art, including but not limited to the use of detergent lysates, sonification and vortexing with glass beads. Once

the nucleic acids have been extracted, the genomic double-stranded DNA is used in the analysis.

In a preferred embodiment, the DNA may be cleaved prior to the treatment, and this may be by any means standard in the state of the art, in particular with methylation-sensitive restriction endonucleases.

In the *third step*, the DNA is then digested with one or more methylation sensitive restriction enzymes. The digestion is carried out such that hydrolysis of the DNA at the restriction site is informative of the methylation status of a specific CpG dinucleotide.

In the *fourth step*, which is optional but a preferred embodiment, the restriction fragments are amplified. This is preferably carried out using a polymerase chain reaction, and said amplicates may carry suitable detectable labels as discussed above, namely fluorophore labels, radionucleotides and mass labels.

In the *fifth step* the amplicates are detected. The detection may be by any means standard in the art, for example, but not limited to, gel electrophoresis analysis, hybridization analysis, incorporation of detectable tags within the PCR products, DNA array analysis, MALDI or ESI analysis.

In the final step of the method the presence, absence or subclass of prostate cell proliferative disorder is deduced based upon the methylation state of at least one CpG dinucleotide sequence of SEQ ID NO 1 to SEQ ID NO 59, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences of SEQ ID NO 1 to SEQ ID NO 59.

Diagnostic assays for prostate cell proliferative disorders

The present invention enables diagnosis of events which are disadvantageous to patients or individuals in which important genetic and/or epigenetic parameters within one or more of SEQ ID NO: 1 to SEQ ID NO: 59 may be used as markers. Said parameters obtained by means of the present invention may be compared to another set of genetic and/or epigenetic parameters, the differences serving as the basis for a diagnosis of events which are disadvantageous to patients or individuals.

Specifically, the present invention provides for diagnostic cancer assays based on measurement of differential methylation of one or more CpG dinucleotide sequences of SEQ ID NO: 1 to SEQ ID NO: 59, or of subregions thereof that comprise such a CpG dinucleotide sequence. Typically, such assays involve obtaining a tissue sample from a test tissue, performing an assay to measure the methylation status of at least one of one or more CpG

dinucleotide sequences of SEQ ID NO: 1 to SEQ ID NO: 59 derived from the tissue sample, relative to a control sample, or a known standard and making a diagnosis or prognosis based thereon.

In particular preferred embodiments, inventive oligomers are used to assess the CpG dinucleotide methylation status, such as those based on SEQ ID NO: 1 to SEQ ID NO: 295, or arrays thereof, as well as in kits based thereon and useful for the diagnosis of prostate cell proliferative disorders.

Kits

Moreover, an additional aspect of the present invention is a kit comprising, for example: a bisulfite-containing reagent; a set of primer oligonucleotides containing at least two oligonucleotides whose sequences in each case correspond, are complementary, or hybridize under stringent or highly stringent conditions to a 16-base long segment of the sequences SEQ ID NO: 1 to SEQ ID NO: 295; oligonucleotides and/or PNA-oligomers; as well as instructions for carrying out and evaluating the described method. In a further preferred embodiment, said kit may further comprise standard reagents for performing a CpG position-specific methylation analysis, wherein said analysis comprises one or more of the following techniques: MS-SNuPE, MSP, MethyLight™, HeavyMethyl™, COBRA, and nucleic acid sequencing. However, a kit along the lines of the present invention can also contain only part of the aforementioned components.

While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following example serves only to illustrate the invention and is not intended to limit the invention within the principles and scope of the broadest interpretations and equivalent configurations thereof.

EXAMPLES

In the following 'uL' is taken to mean 'microlitre' i.e. 10^{-6} litres, accordingly 'uM' is taken to mean 'micromolar'.

Pooled genomic DNA was isolated and analyzed using the discovery methods, AP-PCR and MCA (Example 1). These technologies distinguish between methylated and unmethylated CpG sites through the use of methylation sensitive enzymes. In general, whole genomic DNA is first digested to increase manageability, and then further digested with a methylation sensitive restriction enzyme. Methylated fragments are preferentially amplified because cleavage at the unmethylated sites prevents amplification of these products. Differentially methylated fragments identified using these techniques are sequenced (Example 2) and compared to the human genome using the BLAST utility in the Ensembl database. The sample set was selected based on the initial aim of the diagnostic problem to be solved, namely the improved detection and discrimination of prostate carcinomas from normal or benign conditions. The following comparisons were run using three "All Cancer" prostate cancer sample pools (10,10, and 20 samples each), two benign prostate hyperplasia (BPH) sample pools (10 samples each), three low grade prostate cancer sample pools (10 samples each), three high grade prostate cancer sample pools (10 samples each), and one peripheral blood lymphocytes (PBL) pool (9 samples)]:

- BPH vs. All Cancer (High & low Gleason score; transitional (TZ) and peripheral (PZ) zones, 2 comparisons)
- BPH vs. Low Gleason Score (Gleason < 6, TZ & PZ represented, 2 comparisons)
- BPH vs. High Gleason Score (Gleason > 7, TZ & PZ represented, 2 comparisons)
- Low Gleason Score vs. High Gleason Score (for MCA, each pool was used as tester and driver)
- BPH vs. PBLs
- All cancer vs. PBLs

The BPH vs. PBLs comparison was not done for APPCR.

For all MCA comparisons that included cancer samples, the cancer was the tester. The low to high Gleason score comparison was run twice, once with low as the tester, and once with high

as the tester, bringing the total number of comparisons for MCA to ten. In the experiments with PBLs, the PBL sample was the driver. See Table 1.

Table 1: Sample pools used in comparison studies (AP-PCR and MCA)

Comparison	Nickname	Pool Type	Pool #	Samples per pool	Sample Breakdown			
					Gleas < 6 / Trans. Zone	Gleas < 6 / Periph. Zone	Gleas > 7 Trans. Zone	Gleas > 7 Periph. Zone
BPH vs. All cancers	BA1	BPH	1	10	10 BPH			
		All	1	10	2	3	2	3
BPH vs. All cancers	BA2	BPH	2	10	5 BPH, 5 Normal			
		All	2	10	3	2	3	2
BPH vs. Low	BL1	BPH	1	10	10 BPH			
		Low	1	10	5	5	0	0
BPH vs. Low	BL2	BPH	2	10	5 BPH, 5 Normal			
		Low	2	10	5	5	0	0
BPH vs. High	BH1	BPH	1	10	10 BPH			
		High	1	10	0	0	5	5
BPH vs. High	BH2	BPH	2	10	5 BPH, 5 Normal			
		High	2	10	0	0	5	5
Low vs. High	HL	Low	3	10	5	5	0	0
		High	3	10	0	0	5	5
BPH vs. PBLs	BP	BPH	1	10	10 BPH			
		PBL	1	9	9 PBL's			
Cancer vs. PBL	CP	All	3	20	5	5	5	5
		PBL	1	9	9 PBL's			

Example 1: MCA and AP-PCR

Identifying one or more *primary* differentially methylated CpG dinucleotide sequences using a controlled assay suitable for identifying at least one differentially methylated CpG dinucleotide sequence within the entire genome, or a representative fraction thereof.

All processes were performed on both pooled and/or individual samples, and analysis was carried out using two different Discovery methods; namely, methylated CpG amplification (MCA), and arbitrarily-primed PCR (AP-PCR).

AP-PCR. AP-PCR analysis was performed on sample classes of genomic DNA as follows:

1. DNA isolation; genomic DNA was isolated from sample classes using the commercially available Wizard™ kit;
2. Restriction enzyme digestion; each DNA sample pool was digested with 3 different sets of restriction enzymes for 16 hours at 37°C: RsaI (recognition site: GTAC); RsaI (recognition site: GTAC) plus HpaII (recognition site: CCGG; sensitive to methylation); and RsaI (recognition site: GTAC) plus MspI (recognition site: CCGG; insensitive to methylation);

3. AP-PCR analysis; each of the restriction digested DNA samples was amplified with the primers listed in TABLE 2 at a 40°C annealing temperature, and with ³³P dATP in the primer sets outlined in Table 3.

4. Polyacrylamide Gel Electrophoresis; 1.6 µl of each AP-PCR sample was loaded on a 5% Polyacrylamide sequencing-size gel, and electrophoresed for 4 hours at 130 Watts. Gels were transferred to chromatography paper, covered with saran wrap, and dried in a gel dryer for a period of about 1-hour.

5. Autoradiographic Film Exposure; film was exposed to dried gels for 20 hours at minus 80°C, and then developed. Glogos II Autorad markers (Stratagene) were added to the dried gel and exposure was repeated with new film. The first autorad was retained for records, while the second was used for excising bands; and

6. Bands corresponding to differential methylation were visually identified on the gel. Such bands were excised and the DNA therein was isolated and cloned using the Invitrogen TA Cloning Kit.

Table 2: Primers used according to the AP-PCR Protocol Example 1

Name	SEQ ID NO:	Sequence
GC1	928	GGGCCGCGGC
GC2	929	CCCCGCGGGG
GC3	930	CGCGGGGGCG
GC4	931	GCGCGCCGCG
GC5	932	GCGGGGCGGC
G1	933	GCGCCGACGT
G2	934	CGGGACGCGA
G3	935	CCGCGATCGC
G4	936	TGGCCGCCGA
G5	937	TGCGACGCCG
G6	938	ATCCCGCCCG
G7	939	GCGCATGCGG
G8	940	GCGACGTGCG
G9	941	GCCGCGNGNG
G10	942	GCCCGCGNNG
APBS1	943	AGCGGCCGCG

APBS5	944	CTCCCACGCG
APBS7	945	GAGGTGCGCG
APBS10	946	AGGGGACGCG
APBS11	947	GAGAGGCGCG
APBS12	948	GCCCCGCGA
APBS13	949	CGGGGCGCGA
APBS17	950	GGGGACGCGA
APBS18	951	ACCCACCCG

Table 3

Combination	primer 1	primer 2	primer 3
101	GC1	G2	APBS1
103	GC3	G4	APBS1
105	GC5	G6	APBS1
107	GC2	G8	APBS5
109	GC4	G10	APBS5
111	GC1	G8	APBS7
113	GC3	G6	APBS7
115	GC5	G4	APBS7
117	GC2	G2	APBS10
119	GC4	G2	APBS10
121	GC1	G4	APBS11
123	GC3	G5	APBS11
125	GC5	G7	APBS11
127	GC2	G9	APBS12
129	GC4	G9	APBS12
131	GC1	G7	APBS13
133	GC3	G5	APBS13
135	GC5	G3	APBS13
137	GC2	G1	APBS17
139	GC4	G3	APBS17
141	GC1	G5	APBS18
143	GC3	G7	APBS18
145	GC5	G9	APBS18
147	G2	G3	APBS17
149	G4	G5	APBS17
151	G6	G7	APBS17
153	G8	G9	APBS13
155	G8	G10	APBS13
157	G6	G8	APBS12
159	G4	G6	APBS12

161	G2	G4	APBS12
163	G2	G10	APBS11
165	G2	G5	APBS11
167	G4	G7	APBS10
169	G6	G9	APBS10
171	G1	G8	APBS10
173	G6	G10	APBS7
175	G4	G8	APBS7
177	G2	G6	APBS5
179	G4	G10	APBS5
181	G2	G8	APBS5
183	APBS1	APBS10	APBS11
185	APBS5	APBS7	APBS17
187	APBS1	APBS12	APBS18
189	APBS10	APBS13	APBS17
191	APBS5	APBS11	APBS12
193	APBS7	APBS10	APBS13
195	APBS1	APBS5	APBS11
197	APBS7	APBS17	APBS18
199	APBS1	APBS12	APBS13

MCA. MCA was used to identify hypermethylated sequences in one population of genomic DNA as compared to a second population by selectively eliminating sequences that do not contain the hypermethylated regions. This was accomplished, as described in detail herein above, by digestion of genomic DNA with a methylation-sensitive enzyme that cleaves unmethylated restriction sites to leave blunt ends, followed by cleavage with an isoschizomer that is methylation insensitive and leaves sticky ends. This is followed by ligation of adaptors, amplicon generation and subtractive hybridization of the tester population with the driver population.

The initial restriction digestion reaction solutions contained the following:

DRIVERS:

DNA	510 uL
buffer 4	60 uL
100x BSA	6 uL
SmaI (20U/uL)	24 uL

TESTERS:

DNA	68 uL
buffer 4	10 uL
10x BSA	10 uL
SmaI (20U/uL)	2 uL

The reaction mixtures were incubated overnight at room temperature.

The pools were then further digested with Xma I (2 uL=100 U), 6 hours at 37°C. 2 uL (20U) XmaI was added to each tester digest and 8 uL (80U) to each driver digest

The cleaned-up, digested material was ligated to the adapter-primer RXMA24 + RXMA12 (Sequence: RXMA24: AGCACTCTCCAGCCTCTCACCGAC (SEQ ID NO: 952); RXMA12: CCGGGTCGGTGA (SEQ ID NO:953). These were hybridized to create the adapter by heating together at 70°C and slowly cooling to room temperature (RT) in a 30 uL reaction:

Each DNA	33 uL
T4 Buffer	6 uL
RXMA adapter-primer (100 uM)	20 uL
Ligase	1 uL

The reaction solution was incubated overnight at room temperature.

3 uL of the ligation mix for both tester and driver populations was used in each initial PCR to generate the starting amplicons. The reaction solutions were as follows:

TESTERS

100uM RXMA24	1 uL
PCR buffer	10 uL
25 mM dNTPs	1.2 uL
ddH2O	68.8 uL
Titanium Taq	1 uL
100% DMSO	2 uL
5M Betaine	10 uL

3 uL ligated tester DNA was added to each 97 uL tester cocktail.

DRIVERS

Drivers are amplified with dUTP in place of dTTP:

100uM RXMA24	1 uL
PCR buffer	10 uL
25 mM dNTPs	1.2 uL
(25 mM each dATP, dCTP, dGTP, and dUTP)	
ddH2O	68.8 uL
Titanium Taq	1 uL
100% DMSO	2 uL
5M Betaine	10 uL

3 uL ligated driver DNA was added to each 97 uL driver cocktail.

PCR conditions:

72 degrees 5 min

30 cycles:

95 degrees 1 min

72 degrees 3 min

Final extension:

72 degrees 10 min.

The tester amplicons were then digested with XmaI, yielding overhanging ends, and the driver amplicons were digested with SmaI, yielding blunt end fragments.

DRIVERS (SmaI):

DNA	500 uL
Buffer 4	100 uL
100x BSA	10 uL
H2O	340 uL
SmaI (20U/uL)	50 uL

Total vol: 1 mL. Incubated overnight at room temp.

TESTERS (XmaI):

DNA	20 uL
buffer 4	10 uL
10x BSA	10 uL
H2O	59 uL
XmaI (50U/uL)	1 uL

Total vol: 100 uL. Incubated overnight at 37 degrees.

A new set of adapter primers (hybridized as described for the above RXMA primers) JXMA24 + JXMA12 (Sequence: JXMA24: ACCGACGTCGACTATCCATGAACC (SEQ ID NO:954); JXMA12: CCGGGGTTCATG (SEQ ID NO:955) was ligated to the Tester in a Thermocycler at 16°C for 2 hours in the following reaction solution:

DNA	16 uL
T4 buffer	3 uL
JXMA-P adapter (100uM)	10 uL
T4 Ligase (400U/uL)	1 uL

The digested tester and driver amplicons were hybridized together. A selective PCR reaction was done using primer JXMA24 (SEQ ID NO:954). The reaction solution contained:

JXMA24	0.5 uL
taq buffer	5 uL
dNTPs	0.6 uL
ddH2O	27.4 uL
betaine	5 uL
DMSO	1 uL
Titanium taq	0.5 uL
DNA	10 uL

PCR conditions:

72 degrees 8 min (fill in ends)

5 cycles:

95 degrees 1 min

72 degrees 3 min

final extension:

72 degrees 10 min

Subsequently, 20 uL of Mung Bean nuclease buffer plus 10 uL Mung Bean Nuclease (10U) was added and incubated at 37°C for 30 minutes. This reaction was cleaned up and used as a template for 25 more cycles of PCR using JXMA24 primer in the following reaction solution:

JXMA24	1 uL
taq buffer	10 uL
dNTPs	1.2 uL
ddH2O	27 uL
betaine	10 uL
DMSO	2 uL
Titanium taq	1 uL
DNA	48 uL

under the following conditions.

95 degrees 2 min

30 cycles:

95 degrees 1 min

72 degrees 3 min

Final extension:

72 degrees 10 min

Hold at 4 degrees

The resulting PCR product (tester) was digested again using XmaI:

45 uL DNA

15 uL Buffer 4

15 uL 10x BSA

71 uL H2O

4 uL XmaI

Incubated overnight at 37 degrees

A third adapter, NXMA24 (AGGCAACTGTGCTATCCGAGTGAC; SEQ ID NO:956) + NXMA12 (CCGGGTCACTCG; SEQ ID NO: 957) was ligated. The tester (500 ng) was hybridized a second time to the original digested driver (40 ug) in 4 uL EE (30 mM EPPS, 3 mM EDTA) and 1 uL 5 M NaCl at 67°C for 20 hours. Selective PCR was performed using NXMA24 primer as follows:

NXMA24	0.5 uL
taq buffer	5 uL
dNTPs	0.6 uL
ddH2O	27.4 uL
betaine	5 uL
DMSO	1 uL
Titanium taq	0.5 uL
<u>DNA</u>	<u>10 uL</u>

PCR program:

72 degrees 8 min (fill in ends)

8 cycles:

95 degrees 1 min

72 degrees 3 min

final extension:

72 degrees 10 min

The reaction solution was held at 4 degrees

Subsequently, 20 uL of Mung Bean nuclease buffer plus 10 uL Mung Bean Nuclease (10U) was added and incubated at 30°C for 30 minutes. This reaction was cleaned up and used as a template for 25 more cycles of PCR using NXMA24 primer as follows:

Reaction solution

NXMA24	1 uL
taq buffer	10 uL
dNTPs	1.2 uL

ddH2O	27 uL
betaine	10 uL
DMSO	2 uL
Titanium taq	1 uL
DNA	48 uL

PCR program:

95 degrees 2 min

30 cycles:

95 degrees 1 min

72 degrees 3 min

Final extension:

72 degrees 10 min

Hold at 4 degrees

The resulting PCR product was digested with XmaI :

Reaction solution:

DNA	38 uL
buffer 4	5 uL
10x BSA	5 uL
Xma I	2 uL

Incubated overnight at 37 degrees.

The DNA digest was then ligated into the vector pBC Sk—predigested with XmaI and phosphatased (675 ng). 5 uL of the ligation mixture was used to transform chemically competent TOP10™ cells according to the manufacturer's instructions. The transformations were plated onto LB/XGal/IPTG/CAM plates. Selected insert colonies were sequenced according to Example 2.

Example 1 resulted in a large number of unique sequences that were potential candidates for assay markers. A subset of these sequences was eliminated due their high (>50%) repeat content. A total of 480 unique sequences were identified in the comparisons performed for this study. A subset of these sequences were further selected using the following scoring procedure:

- Appearance using multiple methods
- Appearance in multiple pools
- Located within CpG island
- Located within the promoter region of a gene
- Near or within predicted or known gene
- Known to be associated with disease
- Class of gene (transcription factor, growth factor, etc.)
- Repetitive element (negative score)

Under this scoring scheme, a MeST sequence receives a point for each of the above criteria, and receives a score of (-)8 for having repetitive sequence content greater than 50%. The highest score possible is 7, the lowest is (-)8. Scores are automatically generated using a proprietary database. Of the initial set of 480 MeST sequences, 277 scored 0 or higher. Using the scoring criteria above, along with manual review of the sequences, the number of candidate MeST was further reduced to 126 unique sequences.

Primer design for the 126 sequences was then initiated for the purpose of bisulfite sequencing. Thirty five of the sequences were discarded for various reasons including inability to design adequate primers, failure of amplification from control DNA, or if further scrutiny of the sequence or updates of the Ensembl database revealed poor quality or repeat sequences not previously noted.

Example 2: Bisulfite Sequencing

For bisulfite sequencing amplification primers were designed to cover each identified MeST sequence when possible or part of the 1000 bp upstream or 1000 bp downstream flanking regions surrounding the position. Samples used in Example 1 were utilized for amplicon production in this phase of the study. Each sample was treated with sodium bisulfite and sequenced. Sequence data was obtained using ABI 3700 sequencing technology. Obtained

sequence traces were normalized and percentage methylation calculated using Epigenomic's proprietary ESME bisulphite sequence sequencing trace analysis program.

Results of bisulfite sequencing

The following properties were noted:

1. Bisulfite sequencing indicates differential methylation of a CpG site between selected classes of samples (fisher score)
2. Co-methylation is observed
3. If only one site has Fisher score >1 , are there additional sites surrounding with fisher score > 0.5 ?
4. Are there trends in the pattern?-blocks of blue vs yellow (not necessarily high fisher score)

Genomic regions that were considered to demonstrate significant co-methylation as assessed by these criteria then proceeded to further investigation.

Figures 1 to 3 are ranked matrices produced from bisulfite sequencing data analysed by the Epigenomics' proprietary 'ESME' program. The overall matrix represents the sequencing data for one region of interest. Each row of the matrix is a single CpG site within the fragment and each column is an individual DNA sample. The bar on the left represents a scale of the percent methylation, with the degree of methylation represented by the shade of each position within the column from black representing 100% methylation to light grey representing 0% methylation. No data was available for white positions.

Figure 1 shows the sequencing data of a fragment of the gene Prostaglandin E2 Receptor, EP4 Subtype. Here, bisulfite sequencing showed differential but non-conclusive patterns of methylation between samples. The gene was further investigated on a larger sample set using the array process (Example 3) as the accuracy of this gene as a marker could be improved when analysed in combination with other genes.

Figure 2 shows the sequencing data of a fragment of the gene Orphan Nuclear Receptor (α -1Fetoprotein Transcription Factor). In this case, bisulfite sequencing indicated differential methylation or comethylation between sample types.

Figure 3 shows the sequencing data of a fragment of the gene 1-Acyl-SN-Glycerol-3-Phosphate Acyltransferase Gamma. This was representative , of a subset of ROIs for which only poor quality sequence reads was obtained and the gene was only able to be meaningfully analysed using the array process (Example 3)

Example 3: Array analysis

A selection of the differentially methylated genomic regions were then further analysed by means of high throughput array analysis. The most useful final assay suitable for a diagnostic/classification screening test would enable analysis of body fluids such as serum, plasma or urine sediment (obviating the need for invasive procedures). Therefore, the sample set included DNA samples from other cancers which may be present in blood to provide more specific marker sets for sensitive assays.

Description of sample set for chip study

The sample set for the microarray analysis was designed to provide information concerning both the sensitivity and specificity of the marker candidates. A large number of samples (Table 7) from prostate cancer, BPH and normal prostate were screened. Prostate cancer samples were grouped by Gleason Score (High (≥ 8), Moderate (7), and Low (≤ 6)) and by zone (peripheral or transitional). The distribution of BPH samples was random, but because most BPH is derived from the transitional zone, it can be assumed that most samples were of that origin. In addition to prostate samples, a number of other cancer types were included to test for specificity to the prostate. The proposed samples for the study included the tissues in Table 7. PBL samples were included because of the proposed use of these markers in a blood based screen. Normal liver and liver cancer were also included because of the observed methylation of GSTP1 in these samples.

Sample Type	Sample Type
Prostate Cancers <ul style="list-style-type: none"> • High Grade (Gleason ≥ 8) • Transitional Zone • Peripheral Zone • Low Grade (Gleason ≤ 6) • Transitional Zone • Peripheral Zone • Moderate Grade (Gleason = 7) • Transitional Zone • Peripheral Zone • Additional Prostate Cancers • Post hormone therapy 	Endocrine Related Cancers <ul style="list-style-type: none"> • Breast • Male • Female • Ovarian • Uterine
Benign Prostate Disease <ul style="list-style-type: none"> • BPH • Benign Fibroma • Prostatitis 	Other Cancers <ul style="list-style-type: none"> • Liver • Lung • Esophageal • Salivary Gland • Stomach • Pancreatic • Melanoma • Colon
Genitourinary Tract Cancers <ul style="list-style-type: none"> • Bladder • Testicular • Kidney 	Other Normal tissues <ul style="list-style-type: none"> • Prostate • Transitional • Peripheral • Additional • Bladder • Kidney • Liver • Testes • Sperm • Ureter • PBLs

Table 7. Overview of samples for the array study.

DNA extraction

Samples were received from either as frozen tissue or extracted genomic DNA. All DNA samples were extracted using Qiagen Genomic Tip-500 columns or the MagnaPure device.

Bisulfite treatment and multiplex PCR

Total genomic DNA of all samples was bisulfite treated to convert unmethylated cytosines to uracil. Methylated cytosines remained conserved as cytosines. Bisulfite treatment was performed using Epigenomics' proprietary bisulfite treatment process. Two independent bisulfite reactions were performed per patient sample. After bisulfitation 10 ng of each DNA sample was used in subsequent multiplex PCR (mPCR) reactions containing 7-8 primer pairs.

Hybridization

Each reaction contained the following:

0.4 mM each dNTPS

1 Unit Taq Polymerase

2.5 ul PCR buffer

3.5 mM MgCl₂

80 nM Primerset (12-16 primers)

11.25 ng DNA (bisulfite treated)

Further details of the primers are shown in TABLE 8.

Forty cycles were carried out as follows: Denaturation at 95°C for 15 min, followed by annealing at 55°C for 45 sec., primer elongation at 65°C for 2 min. A final elongation at 65°C was carried out for 10 min.

Hybridization

All PCR products from each individual sample were then hybridised to glass slides carrying a pair of immobilised oligonucleotides for each CpG position under analysis. Each of these detection oligonucleotides was designed to hybridise to the bisulphite converted sequence around one CpG site which was either originally unmethylated (TG) or methylated (CG). See Table 2 for further details of all hybridisation oligonucleotides used (both informative and non-informative.) Hybridisation conditions were selected to allow the detection of the single nucleotide differences between the TG and CG variants.

5 ul volume of each multiplex PCR product was diluted in 10 x Ssarc buffer. The reaction mixture was then hybridised to the detection oligonucleotides as follows.

Denaturation at 95°C, cooling down to 10°C, hybridisation at 42°C overnight followed by washing with 10 x SSARC and dH₂O at 42°C.

Further details of the hybridisation oligonucleotides are shown in TABLE 9.

Fluorescent signals from each hybridised oligonucleotide were detected using genepix scanner and software. Ratios for the two signals (from the CG oligonucleotide and the TG oligonucleotide used to analyse each CpG position) were calculated based on comparison of intensity of the fluorescent signals.

For each patient, 2 DNA aliquots were bisulfite treated and for each bisulfite treated DNA sample two hybridizations were performed, resulting in a total of 4 chips processed per patient. For hybridization, the samples were grouped into 2 processing rounds in order to avoid a potential process-bias. As stated, each of the 2 rounds included a 2 fold redundancy for each DNA sample for the 4-fold redundancy per patient. The samples were hybridized in batches of 112 samples randomized for sex, diagnosis, tissue, and bisulfite batch .

Data analysis methods

Analysis of the chip data

For the analysis of the chip data Epigenomics' proprietary software "EpiScape" was used. It encompasses a variety of statistical tools and novel machine learning methods for analyzing and visualizing methylation array data. In the following sections we summarize the most important data analysis techniques that we applied for analyzing the data.

From raw hybridization intensities to methylation ratios

- The log methylation ratio ($\log(\text{CG}/\text{TG})$) at each CpG position is determined according to a standardized preprocessing pipeline. This log ratio has the property that the hybridization noise has approximately constant variance over the full range of possible methylation rates.

Hypothesis testing

Our main task was to identify markers that can make a significant contribution to the class prediction of samples. For the 'particularly preferred embodiments' of the invention the significant contribution is detected when the null-hypothesis that a prediction model including the marker does not improve classification performance over a model without the marker can be rejected with $p < 0.05$. Because we apply this test to a whole set of potential markers, we corrected the p-values for multiple testing. We did this by applying the conservative

Bonferroni correction, which simply multiplies the single marker p-values with the number of potential markers tested. We also give results with the less conservative False Discovery Rate (FDR) method.

Throughout this example a marker (sometimes also simply referred to as gene or amplicon) is also referred to as a genomic region of interest (ROI). It comprises of several CpG positions in the respective genomic region. For testing the null hypothesis that a marker has no predictive power we use the likelihood ratio test for logistic regression models. The logistic regression model for a single marker is a linear combination of methylation measurements from all CpG positions in the respective ROI. The fitted logistic regression model is compared to a constant probability model that is independent of methylation and represents the null hypothesis. The p-value of the marker is computed via the likelihood ratio test.

A significant p-value for a marker means that the methylation of this ROI has some systematic correlation to the question of interest as given by the two classes. In general a significant p-value does not necessarily imply a good classification performance. However, because with logistic regression we use a linear predictor as the basis of our test statistic small p-values will be indicative of a good clinical performance.

Class prediction by supervised learning

In order to give a reliable estimate of how well the CpG ensemble of a selected marker can differentiate between different tissue classes we can determine its prediction accuracy by classification. For that purpose we calculated a methylation profile-based prediction function using a certain set of tissue samples with a specific class label. This step is called training and it exploits the prior knowledge represented by the data labels. The prediction accuracy of that function is then tested on a set of independent samples. As a method of choice, we use the support vector machine (SVM) algorithm to learn the prediction function. In this analysis, sensitivity and specificity were weighted equally. This is achieved by setting the risk associated with false positive and false negative classifications to be inversely proportional to the respective class sizes. Therefore sensitivity and specificity of the resulting classifier can be expected to be approximately equal. Note that this weighting can be adapted according to the clinical requirements.

Estimating the performance of the tissue class prediction: Cross Validation

With limited sample size the cross-validation method provides an effective and reliable estimate for the prediction accuracy of a discriminator function, and therefore in addition to

the significance of the markers we provide cross-validation accuracy, sensitivity and specificity estimates. For each classification task, the samples were partitioned into 5 groups of approximately equal size. Then the learning algorithm was trained on 4 of these 5 sample groups. The predictor obtained by this method was then tested on the remaining group of independent test samples. The number of correct positive and negative classifications was counted over 10 runs for the learning algorithm for all possible choices of the independent test group without using any knowledge obtained from the previous runs. This procedure was repeated on 10 random permutations of the sample set giving a better estimate of the prediction performance than if performed by simply splitting the samples into one training sample set and one independent test set.

Data analysis results

Our first step in analysis of the array data was to look at discriminatory markers in a comparison of all tissues of prostatic origin. We first compared normal and BPH prostate tissue against prostate cancer samples, and found that many of the markers used in this study have p-values meeting the desired criteria (Figure 4). Next, we compared prostate cancer tissues to all other tissue classes used in this study (Table 7). Almost all markers met the specified statistical criteria with this sample set. The GSTP1 gene is known to be hypermethylated in prostate cancer, but also displays hypermethylation in other cancers. Therefore, our final comparison was a more detailed examination of the methylation levels in prostate cancer versus other cancer types.

Prostate Normal and BPH vs. Prostate Cancer

In this comparison, the negative class consists of 91 samples from normal prostate, and BPH. The positive class consists of 99 prostate cancer samples. Most of the markers meet the criteria of p-value < 0.05 (Figure 4). The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 4. The best 12 markers are further shown in Figure 5.

Prostate Normal and Other Tissues vs. Prostate Cancer

Comparisons were then performed on the complete sample set. The negative group was expanded to include normal tissue from other organs and cancer of other origins than prostate,

according to table 7. The negative class consists of 254 samples from normal prostate, BPH and other normal and cancerous tissues. The positive class consists of 99 prostate cancer samples. Again the p-values for most markers meet the significance level of $p = < 0.05$ (Table 5). The accuracy of the highest performing marker is ~ 86% (see figure 6 and/or table 5). The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 5. The best 12 markers are further shown in Figure 7.

Other Cancers vs. Prostate Cancer

Since hypermethylation of GSTP1 (state of the art methylation prostate cancer marker) is not specific to the prostate, we examined the methylation status of prostate cancer and other cancers in greater detail. Figure 16 shows that GSTP1 (SEQ ID NO:57) was strongly hypermethylated in liver cancer and to a lesser degree in breast cancer. Nevertheless, several other of the best candidate markers distinguish well between cancer of the prostate and liver. The p-values, accuracy, sensitivity and specificity of the analysis are shown in Table 5. The best 12 markers are further shown in Figure 8.

Tables 4-6 below summarize the performance characteristics of all markers in the following comparisons:

Normal Prostate and BPH vs. Prostate Cancer (Table 4)

Normal Prostate, BPH and other tissues vs. Prostate Cancer (Table 5)

Other Tissues vs. Prostate Cancer (Table 6)

The analyses in tables 4 and 5 contained BPH and normal prostate samples in the analysis group. The analysis for Normal Prostate and BPH vs. Prostate Cancer was designed to determine the performance of the markers in a prostate specific environment. The analysis that included other tissues, both cancer and normals (Normal Prostate, BPH and Other Tissues vs. Prostate Cancer) took into consideration the performance of the markers with a background that may contribute or alter the overall performance of the markers in remote samples.

Cancer types (table 6) were also compared because of the propensity for GSTP1 to be methylated in multiple cancer types. This type of lack of specificity could have a negative impact on the performance of a marker in body fluid-based assays. GSTP1 (SEQ ID NO: 57) is highly methylated in prostate cancer, but also in liver cancer as anticipated. IGF2 (SEQ ID NO: 58) is similarly methylated in liver cancer. The majority of the markers shown in Figure 8 are unmethylated in most cancer types, with the exception of prostate cancer. From Figures 4-8, it can be observed that there are multiple candidates that have the potential to be informative and accurate

markers. It is recommended that multiple markers be combined to ensure a high sensitivity and specificity.

Table 4: Normal Prostate, BPH and Other Tissues vs. Prostate Cancer

Genomic SEQ ID NO:	Treated Methylated sense strand SEQ ID NO:	Treated Methylated Antisense strand SEQ ID NO:	Treated Unmethylated strand SEQ ID NO:	Treated Unmethylated antisense sense strand SEQ ID NO:	P-value	Accuracy	Sensitivity	Specificity
57	172	173	290	291	1.30E-027	0.86	0.67	0.93
23	104	105	222	223	2.00E-029	0.81	0.75	0.83
36	130	131	248	249	3.80E-018	0.75	0.75	0.76
56	170	171	288	289	1.10E-012	0.74	0.62	0.79
11	80	81	198	199	5.10E-019	0.74	0.76	0.74
20	98	99	216	217	4.90E-016	0.73	0.77	0.71
22	102	103	220	221	1.10E-009	0.7	0.61	0.74
31	120	121	238	239	6.90E-018	0.7	0.79	0.66
30	118	119	236	237	1.60E-012	0.69	0.81	0.64
58	174	175	292	293	1.20E-011	0.68	0.71	0.67
34	126	127	244	245	5.50E-009	0.68	0.65	0.69
41	140	141	258	259	1.50E-008	0.67	0.7	0.66
59	176	177	294	295	4.90E-007	0.67	0.59	0.7
51	160	161	278	279	1.50E-012	0.67	0.76	0.63
24	106	107	224	225	1.30E-006	0.67	0.67	0.67
18	94	95	212	213	1.10E-014	0.67	0.84	0.6
54	166	167	284	285	3.80E-007	0.66	0.7	0.65
27	112	113	230	231	6.60E-007	0.66	0.7	0.64
7	72	73	190	191	8.30E-005	0.65	0.62	0.67
35	128	129	246	247	1.00E-004	0.65	0.53	0.69
16	90	91	208	209	7.50E-011	0.64	0.77	0.8
38	134	135	252	253	1.20E-004	0.64	0.63	0.64
14	86	87	204	205	5.20E-008	0.63	0.72	0.6
25	108	109	226	227	3.50E-011	0.62	0.79	0.58
1	60	61	178	179	8.20E-005	0.62	0.67	0.6
28	114	115	232	233	1.40E-003	0.62	0.67	0.59
43	144	145	262	263	3.70E-002	0.61	0.58	0.63
4	66	67	184	185	4.40E-004	0.61	0.64	0.59
26	110	111	228	229	5.60E-003	0.6	0.64	0.59
12	82	83	200	201	3.00E-004	0.58	0.75	0.52
21	100	101	218	219	1.80E-002	0.57	0.64	0.54
33	124	125	242	243	1.10E-002	0.56	0.66	0.53

Table 5: Normal Prostate and BPH vs. Prostate Cancer

Genomic SEQ ID NO:	Treated methylated sense strand SEQ ID NO:	Treated methylated antisense strand SEQ ID NO:	Treated unmethylated sense strand SEQ ID NO:	Treated unmethylated antisense strand SEQ ID NO:	P-value	Acc	Sens	Specificity
57	172	173	290	291	4.60E-023	0.85	0.77	0.93
36	130	131	248	249	8.10E-019	0.81	0.75	0.86
23	104	105	222	223	6.10E-019	0.8	0.75	0.85
34	126	127	244	245	3.10E-015	0.78	0.71	0.86
20	98	99	216	217	1.60E-016	0.78	0.75	0.8
31	120	121	238	239	5.20E-015	0.76	0.71	0.81
59	176	177	294	295	1.90E-014	0.76	0.68	0.84
56	170	171	288	289	2.00E-013	0.76	0.65	0.53
30	118	119	236	237	5.90E-011	0.75	0.76	0.75
48	154	155	272	273	2.70E-011	0.74	0.71	0.78
54	166	167	284	285	1.20E-009	0.74	0.72	0.76
11	80	81	198	199	1.00E-010	0.74	0.69	0.8
24	106	107	224	225	1.10E-011	0.72	0.67	0.78
14	86	87	204	205	3.50E-009	0.71	0.63	0.8
18	94	95	212	213	3.10E-010	0.71	0.76	0.66
28	114	115	232	233	7.80E-008	0.71	0.69	0.72
8	74	75	192	193	4.10E-008	0.7	0.72	0.68
7	72	73	190	191	3.00E-004	0.7	0.62	0.78
4	66	67	184	185	6.30E-009	0.69	0.66	0.72
35	128	129	246	247	1.40E-008	0.69	0.59	0.8
27	112	113	230	231	1.40E-006	0.69	0.68	0.7
58	174	175	292	293	8.90E-006	0.68	0.65	0.71
26	110	111	228	229	1.20E-008	0.68	0.69	0.66
22	102	103	220	221	3.40E-008	0.67	0.57	0.78
41	140	141	258	259	7.90E-005	0.66	0.67	0.66
37	132	133	250	251	1.70E-006	0.66	0.6	0.73
1	60	61	178	179	7.40E-005	0.66	0.72	0.6
49	156	157	274	275	1.80E-005	0.66	0.62	0.71
16	90	91	208	209	1.30E-003	0.65	0.67	0.62
2	62	63	180	181	1.50E-002	0.64	0.66	0.63
44	146	147	264	265	7.50E-004	0.64	0.67	0.6
32	122	123	240	241	2.50E-003	0.64	0.59	0.69
13	84	85	202	203	5.10E-002	0.63	0.61	0.66
47	152	153	270	271	2.00E-002	0.63	0.64	0.61
42	142	143	260	261	3.30E-003	0.62	0.67	0.57
55	168	169	286	287	7.10E-003	0.62	0.67	0.57
29	116	117	234	235	5.10E-002	0.62	0.64	0.59
3	64	65	182	183	1.30E-001	0.61	0.59	0.64
50	158	159	276	277	1.00E+000	0.6	0.64	0.56
51	160	161	278	279	2.90E-002	0.6	0.65	0.56
43	144	145	262	263	9.60E-002	0.6	0.6	0.61
21	100	101	218	219	6.20E-001	0.59	0.66	0.52
46	150	151	268	269	3.00E-001	0.59	0.59	0.59
10	78	79	196	197	5.50E-001	0.59	0.52	0.66
38	134	135	252	253	5.10E-001	0.58	0.55	0.62
25	108	109	226	227	1.20E-002	0.57	0.52	0.63

15	88	89	206	207	1.00E+000	0.56	0.48	0.65
6	70	71	188	189	1.00E+000	0.56	0.63	0.48
33	124	125	242	243	1.00E+000	0.55	0.43	0.68
5	68	69	186	187	1.00E+000	0.55	0.6	0.5
9	76	77	194	195	1.00E+000	0.55	0.53	0.56
52	162	163	280	281	1.00E+000	0.54	0.48	0.6
40	138	139	256	257	1.00E+000	0.53	0.48	0.58
45	148	149	266	267	1.00E+000	0.52	0.38	0.68
17	92	93	210	211	1.00E+000	0.52	0.58	0.46
12	82	83	200	201	1.00E+000	0.47	0.36	0.58
39	136	137	254	255	1.00E+000	0.45	0.46	0.45
19	96	97	214	215	1.00E+000	0.4	0.46	0.32

Table 6: Other cancers vs. Prostate cancer

Genomic SEQ ID NO:	Treated methylated sense strand SEQ ID NO:	Treated methylated antisense strand SEQ ID NO:	Treated unmethylated sense strand SEQ ID NO:	Treated unmethylated antisense strand SEQ ID NO:	p-value	accuracy	sensitivity	specificity
57	172	173	290	291	9.7e-14	0.80	0.70	0.89
23	104	105	222	223	2.4e-19	0.78	0.75	0.81
25	108	109	226	227	6.9e-16	0.75	0.85	0.65
11	80	81	198	199	2.0e-13	0.75	0.76	0.73
51	160	161	278	279	2.0e-12	0.74	0.79	0.69
31	120	121	238	239	1.5e-13	0.74	0.92	0.58
16	90	91	208	209	1.1e-14	0.73	0.82	0.66
30	118	119	236	237	2.4e-08	0.73	0.82	0.64
10	78	79	196	197	5.5e-11	0.72	0.83	0.63
41	140	141	258	259	9.4e-07	0.70	0.73	0.66
18	94	95	212	213	5.0e-09	0.69	0.83	0.57
14	86	87	204	205	2.8e-09	0.69	0.86	0.55
20	98	99	216	217	9.2e-07	0.68	0.78	0.60
12	82	83	200	201	9.7e-07	0.68	0.76	0.61
36	130	131	248	249	6.1e-08	0.67	0.74	0.62
38	134	135	252	253	3.8e-05	0.67	0.66	0.69
22	102	103	220	221	4.1e-05	0.67	0.62	0.71
58	174	175	292	293	1.6e-08	0.66	0.73	0.61
46	150	151	268	269	6.6e-08	0.66	0.87	0.48
56	170	171	288	289	4.6e-05	0.66	0.60	0.72
27	112	113	230	231	1.4e-02	0.65	0.69	0.62
21	100	101	218	219	5.6e-05	0.64	0.70	0.59
15	88	89	206	207	4.5e-05	0.63	0.85	0.43
5	68	69	186	187	4.4e-06	0.63	0.73	0.54
42	142	143	260	261	2.8e-04	0.62	0.77	0.49
34	126	127	244	245	6.8e-03	0.62	0.70	0.55
7	72	73	190	191	3.0e-03	0.62	0.56	0.66
33	124	125	242	243	7.6e-02	0.61	0.72	0.52
28	114	115	232	233	7.2e-01	0.60	0.73	0.49
6	70	71	188	189	2.8e-01	0.60	0.65	0.55

1	60	61	178	179	9.5e-02	0.59	0.60	0.58
59	176	177	294	295	5.1e-02	0.59	0.62	0.56
43	144	145	262	263	4.2e-01	0.59	0.58	0.60
24	106	107	224	225	1.3e-01	0.59	0.76	0.43
37	132	133	250	251	1.1e-01	0.59	0.69	0.49
48	154	155	272	273	5.8e-01	0.59	0.72	0.47
4	66	67	184	185	4.2e-02	0.58	0.71	0.48
45	148	149	266	267	1.0e+00	0.58	0.79	0.40
39	136	137	254	255	3.1e-02	0.58	0.55	0.61
55	168	169	286	287	1.0e+00	0.58	0.69	0.48
26	110	111	228	229	7.3e-02	0.58	0.67	0.49
2	62	63	180	181	1.0e+00	0.57	0.63	0.52
54	166	167	284	285	8.2e-01	0.57	0.68	0.47
49	156	157	274	275	5.9e-02	0.56	0.82	0.34
8	74	75	192	193	1.0e+00	0.56	0.61	0.51
13	84	85	202	203	1.0e+00	0.56	0.59	0.53
32	122	123	240	241	1.0e+00	0.55	0.63	0.49
29	116	117	234	235	1.0e+00	0.55	0.55	0.55
19	96	97	214	215	1.0e+00	0.55	0.54	0.55
47	152	153	270	271	1.0e+00	0.54	0.84	0.29
9	76	77	194	195	9.7e-02	0.54	0.55	0.53
50	158	159	276	277	1.0e+00	0.54	0.62	0.47
52	162	163	280	281	1.0e+00	0.54	0.51	0.56
17	92	93	210	211	1.0e+00	0.54	0.49	0.57
44	146	147	264	265	1.0e+00	0.53	0.60	0.47
35	128	129	246	247	1.0e+00	0.52	0.45	0.59
3	64	65	182	183	1.0e+00	0.52	0.59	0.45
40	138	139	256	257	1.0e+00	0.51	0.56	0.47

TABLE 8

SEQ ID No:	Primer:	Amplificate Length:
(SEQ ID NO: 1)	TGGTATAGGAGGAGAAGAGTTG (SEQ ID NO: 296) TCAATCCCTAAAACCCAAA (SEQ ID NO: 297)	327
(SEQ ID NO: 2)	ACCCAAACTAACAATCAAAAAT (SEQ ID NO: 299) GGAAGGGAAGGATGAGAGTAT (SEQ ID NO: 298)	326
(SEQ ID NO: 3)	GGAAGGTTTAAGGTGAGAGAA (SEQ ID NO: 300) CAAATAACCAATCCCCTAAA (SEQ ID NO: 301)	339
LIM/HOME BOX PROTEIN	CCCCAATATAAATCTACCAACC (SEQ ID NO: 303) TTATTTGAATTTTGGAGGTTATG	372

SEQ ID No:	Primer:	Amplificate Length:
LHX9 (SEQ ID NO: 4)	(SEQ ID NO: 302)	
(SEQ ID NO: 5)	TTAATGAAGTAGGGTTTGTATTGT (SEQ ID NO: 304) CCTCCAAAATCTTAACCAAAT (SEQ ID NO: 305)	421
(SEQ ID NO: 6)	CCCAACTAACTCAAATTCCAC (SEQ ID NO: 307) TTTATTTTAGGAGGGAAGGATT (SEQ ID NO: 306)	434
(SEQ ID NO: 7)	GTGGTTTTGGGGAATTAGTAT (SEQ ID NO: 308) CTCCTACATATCCCATCTCATC (SEQ ID NO: 309)	483
UBIQUITIN- LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	AATTAAGGTTTAGGGTTTTGTTT (SEQ ID NO: 310) ACCTTCCCTACAAATCTACCTAC (SEQ ID NO: 311)	365
BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN	ATAGTTTTGTGGGTTTAAGAGG (SEQ ID NO: 312) ACCCTAACCTTATACAATACCAAC (SEQ ID NO: 313)	414

SEQ ID No:	Primer:	Amplificate Length:
(SEQ ID NO: 9)		
BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGTGGGGTTATTAAGGAGTTTA (SEQ ID NO: 314) CTCAACTACCATACCCAAAAA (SEQ ID NO: 315)	480
(SEQ ID NO: 10)	TTGTGTTGGTTGTAAAAGGA (SEQ ID NO: 316) CAAACACTATACACCTCTCAACA (SEQ ID NO: 317)	428
(SEQ ID NO: 11)	TTGAGGTTATTGGTTTATAGATTTT (SEQ ID NO: 318) CCCTAACCACCCCTTCTA (SEQ ID NO: 319)	457
(SEQ ID NO: 12)	ACTCCATACACTTTTACCAACC (SEQ ID NO: 321) TGTGTGAAATGTTTTAGTTTAATTG (SEQ ID NO: 320)	455
HOOK2 PROTEIN (SEQ ID NO: 13)	TGTGTTAGGAATGATTGGGTA (SEQ ID NO: 322) AATTTCAAACCAAAATCACC (SEQ ID NO: 323)	461
(SEQ ID NO: 14)	AATTACCAAACCAATTCCTCTTA (SEQ ID NO: 325) GGTTGGGATTTTAGTGTGTG (SEQ ID NO: 324)	366
(SEQ ID NO: 14)	TTATTTGAGGGATTTATTGGAG (SEQ ID NO: 326) CCTTATTAAAACTTACCACCCTAT (SEQ ID NO: 327)	382
(SEQ ID NO: 15)	GTGGGTTAGTGGGAGGTTAT (SEQ ID NO: 328) TAAAAACCCTTCCTACCTCTTA (SEQ ID NO: 329)	440
(SEQ ID NO: 16)	AGATGGGTATGTATTTTGGGTT (SEQ ID NO: 330) ACTAAACTCAACCACCTCACTAA (SEQ ID NO: 331)	181
(SEQ ID NO: 17)	TTTTGGTTAGTTTTATGGGGTA (SEQ ID NO: 332) CACTACTTCAAATCCATCATCA (SEQ ID NO: 333)	484

SEQ ID No:	Primer:	Amplificate Length:
LYSOSOMA L- ASSOCIATE D MULTITRAN SMEMBRAN E PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TAACTTCACAAATTACCCAACA (SEQ ID NO: 335) AAGAGTGAGGAGTAAGGGAGTT (SEQ ID NO: 334)	455
"TYPE I INOSITOL- 1,4,5- TRISPHOSP HATE 5- PHOSPATA SE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	TTTTGGGGTTAGTATGTGAGTT (SEQ ID NO: 336) ATCCCAACAACCTCTTCCTC (SEQ ID NO: 337)	482
PROSTAGLA NDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOI D EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GAAGAGGAATGGGAAAATTAG (SEQ ID NO: 338) TCACCAACAAAATACCCAA (SEQ ID NO: 339)	500
PROSTAGLA NDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOI D EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AACCATCAACCATACCTATTTC (SEQ ID NO: 341) TGAGTAAGATGATTATTTGGATTT (SEQ ID NO: 340)	467

SEQ ID No:	Primer:	Amplificate Length:
EP4 SUBTYPE) (SEQ ID NO: 20)		
(SEQ ID NO: 21)	CACTTCCCACCTCCTTATATC (SEQ ID NO: 343) ATTGGGTTTGAAAGAGTTGTAG (SEQ ID NO: 342)	398
(SEQ ID NO: 22)	ATGATGGGAATATGTAAGAATGA (SEQ ID NO: 344) CTTCTCACTACTAATCTCCTACCC (SEQ ID NO: 345)	290
EQUILIBRA TIVE NUCLEOSID E TRANSPORT ER 1 (EQUILIBRA TIVE NITROBENZ YLMERCAP TOPURINE RIBOSIDE- SENSITIVE NUCLEOSID E TRANSPORT ER) (EQUILIBRA TIVE NBMPR- SENSITIVE NUCLEOSID E TRANSPORT ER) (NUCLEOSI DE TRANSPORT ER, ES-TYPE (SEQ ID NO: 23)	GAGTTGGAGGGTTTTGTTTAA (SEQ ID NO: 346) CAAACCTCCATAAAATTCATCT (SEQ ID NO: 347)	410
ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTE IN	CCACTCACTCAACCCATAA (SEQ ID NO: 349) GTGTGAGGTTTGGGTATTTTT (SEQ ID NO: 348)	398

SEQ ID No:	Primer:	Amplificate Length:
TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)		
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	GATGGTGGGTAGTGTTGTTTAT (SEQ ID NO: 350) AAAACCTATCTACACCTTTCTCTT (SEQ ID NO: 351)	378
(SEQ ID NO: 26)	ATCCCAACCAAAACCTCTAC (SEQ ID NO: 353) AATTAGAGAAGGTAAATGGGTT (SEQ ID NO: 352)	300
(SEQ ID NO: 27)	AATAACTCCAACCTTTCCTCCC (SEQ ID NO: 355) GGGATTTGGGAATTTATTGT (SEQ ID NO: 354)	237
(SEQ ID NO: 27)	GGTGGATGAGTAGTTTGAAGTTT (SEQ ID NO: 356) AAAAACCCCTTTCCTCT (SEQ ID NO: 357)	427
(SEQ ID NO: 28)	GTTGGGGTTTAGTAATTGAAAA (SEQ ID NO: 358) ACCAACACAACTAACACTTACAT	404

SEQ ID No:	Primer:	Amplificate Length:
	(SEQ ID NO: 359)	
PEROXISOM AL MEMBRANE PROTEIN PEX14 (PEROXIN- 14) (PEROXISO MAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	AAGAGGTTTTATGGTGTGAG (SEQ ID NO: 360) CACTCCCTTCCCAAACCTATAC (SEQ ID NO: 361)	473
HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (SEQ ID NO: 30)	CTCCTCAATTCTCACCAAAA (SEQ ID NO: 363) GTGGAAAAAGGAGAGTAAATTG (SEQ ID NO: 362)	356
LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	AAACCCTACTTCCTACAAACAA (SEQ ID NO: 365) AGGGAGGTTTGGTGTATTTT (SEQ ID NO: 364)	420
LOW AFFINITY IMMUNOGL OBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC- GAMMA-	CAATCCCCTTAAAACAAACC (SEQ ID NO: 367) GGAAAGGATAGGATGTTGGAT (SEQ ID NO: 366)	500

SEQ ID No:	Primer:	Amplificate Length:
RIIA) (CD32) (CDW32) (SEQ ID NO: 32)		
1-ACYL-SN- GLYCEROL- 3- PHOSPHATE ACYLTRAN SFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRAN SFERASE 3) (1-AGPAT 3) (LYSOPHOS PHATIDIC ACID ACYLTRAN SFERASE- GAMMA) (LPAAT- GAMMA) (1- ACYLGLYC EROL-3- PHOSPHATE O- ACYLTRAN SFERASE 3) (SEQ ID NO: 33)	CACAATTTCCCACAAAACA (SEQ ID NO: 369) TTAGGGAGATGAGATTAAAGGA (SEQ ID NO: 368)	379
HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TATATGGGGTGGGAGTATTTT (SEQ ID NO: 370) CCTTCCCCTCCTTCTTATACT (SEQ ID NO: 371)	276
(SEQ ID NO: 35)	AAAATTCTTTCCTCTCCTAAACA (SEQ ID NO: 373) TTAGGGGTATTAGGTTAAATGA (SEQ ID NO: 372)	478
HISTONE H4 (SEQ ID NO: 36)	TTAGTTGAGAAAGTGGGGGT (SEQ ID NO: 374) CTACCTCAAACCAAATCCTC (SEQ ID NO: 375)	421
POTASSIUM VOLTAGE- GATED CHANNEL SUBFAMILY	TTTTGGAGTTATAGGGTTTGT (SEQ ID NO: 376) CTTCAACATCTCCCAATCC (SEQ ID NO: 377)	441

SEQ ID No:	Primer:	Amplificate Length:
KQT MEMBER 2 (NEUROBLA STOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)		
ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA- ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA- 1B SUBUNIT) (GOLGI ADAPTOR HA1/API ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	AAACCTAAAAATCCAACACAAA (SEQ ID NO: 379) GGGTTATGTTAAGGGAGAAAG (SEQ ID NO: 378)	215
(SEQ ID NO: 39)	AATAACCTAATCTCCAAACCC (SEQ ID NO: 381) ATTTGTGGTAGTTAATAGGTATGTTT A (SEQ ID NO: 380)	465

SEQ ID No:	Primer:	Amplificate Length:
(SEQ ID NO: 40)	TACCCACCATATACCAAACTAAA (SEQ ID NO: 383) TAGAGAAGTTGTTTGTGTTG (SEQ ID NO: 382)	484
PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPL ASTIC PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	ATTTGAGGGGTATTATTGTTG (SEQ ID NO: 384) AACCACCTTCTCCCCTAAT (SEQ ID NO: 385)	409
(SEQ ID NO: 42)	GTAATAATTGGGTTAGGGGTTA (SEQ ID NO: 386) AACCAATATCAAATACTAAAATCC (SEQ ID NO: 387)	394
(SEQ ID NO: 43)	AAAATCCAATCCTAAAACCCTA (SEQ ID NO: 389) TATTTGAGAAAGTGGTAGGAGG (SEQ ID NO: 388)	296
(SEQ ID NO: 44)	AACCCTAACTTCTAAACAATTCC (SEQ ID NO: 391) TTTATGTTTGTGTTGGGGGTAGT (SEQ ID NO: 390)	492
(SEQ ID NO: 45)	ACCCCAATCAACTACATACTAA (SEQ ID NO: 393) GTGAGAGTGGGTGTTGAAAT (SEQ ID NO: 392)	498
(SEQ ID NO: 46)	GAAGGTAGGTTAGTAAGAAGGGT (SEQ ID NO: 394) TACCTAATCCCCCAAACA (SEQ ID NO: 395)	289
(SEQ ID NO: 47)	CACTCACTTAATCATCACCATC (SEQ ID NO: 397) GGAGGAGTTGGGAGTTAGTAT (SEQ ID NO: 396)	459
(SEQ ID NO: 48)	TGATTTGATTAGTTTGGTATTGTT (SEQ ID NO: 398) CAAACACCCCTTAACCCT (SEQ ID NO: 399)	454
(SEQ ID NO: 49)	TAGTGTGTTTGGTTAGAGTGGT (SEQ ID NO: 400) ACACATCTTAAACTTCCCA (SEQ ID NO: 401)	249
DNA REPLICATIO	AACCAACACCTCCTAAACAAT (SEQ ID NO: 403)	412

SEQ ID No:	Primer:	Amplificate Length:
N FACTOR; DOUBLE PARKED, DROSOPHIL A, HOMOLOG OF (SEQ ID NO: 50)	GTTGGGTTTATTTTGAGTTGAG (SEQ ID NO: 402)	
PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIP TION FACTOR MEL1) (SEQ ID NO: 51)	TTGTTTGTTTTGAGTAAGAAGG (SEQ ID NO: 404) ATACCCCAATAACCACCTCTAT (SEQ ID NO: 405)	475
TUMOR SUPPRESSIN G SUBTRANSF ERABLE CANDIDATE 5; P45 BECKWITH- WIEDEMAN N REGION 1A; BECKWITH- WIEDEMAN N SYNDROME CHROMOSO ME REGION 1, CANDIDATE A; EFFLUX TRANSPORT ER-LIKE PROTEIN; ORGANIC CATION TRANSPORT ER-LIKE 2; TUMOR- SUPPRESSIN G STF CDNA 5;	ACCAATCTAAAAATCCCAAC (SEQ ID NO: 407) GGTATTAGGAGGTAGAAGTGGA (SEQ ID NO: 406)	474

SEQ ID No:	Primer:	Amplificate Length:
IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIF IC TRANSPORT ER- RELATED PROTEIN (SEQ ID NO: 52)		
CDH1 (SEQ ID NO: 54)	GAGGTTGGGGTTAGAGGAT (SEQ ID NO: 408) CAAAC TCACAAATACTTTACAATTC (SEQ ID NO: 409)	478
CD44 (SEQ ID NO: 56)	GAAAGGAGAGGTTAAAGGTTG (SEQ ID NO: 410) AACTCACTTAACTCCAATCCC (SEQ ID NO: 411)	696
GSTP1 (SEQ ID NO: 57)	CCTCTCCCCTACCCTATAAA (SEQ ID NO: 413) GTTGGTTTTATGTTGGGAGTT (SEQ ID NO: 412)	469
VIAAT (SEQ ID NO: 59)	CAAACCCAATTCTCAATATCC (SEQ ID NO: 415) GAAGTTGTTGTATATGAGGTTGTTA (SEQ ID NO: 414)	434

TABLE 9

No:	Gene	Oligo:
1	VIAAT (SEQ ID NO: 59)	TAGACGCGGACGTTTA (SEQ ID NO: 416)
2	VIAAT (SEQ ID NO: 59)	TAATTAGATGTGGATGTT (SEQ ID NO: 417)
3	VIAAT (SEQ ID NO: 59)	TTCGTATAGGTACGCGA (SEQ ID NO: 418)
4	VIAAT (SEQ ID NO: 59)	TTTTGTATAGGTATGTGA (SEQ ID NO: 419)
5	VIAAT (SEQ ID NO: 59)	TTCGTACGCGTATTAT (SEQ ID NO: 420)
6	VIAAT (SEQ ID NO: 59)	GAGTTTTGTATGTGTATT (SEQ ID NO: 421)
7	VIAAT (SEQ ID NO: 59)	TTCGGTCGTTTAGCGT (SEQ ID NO: 422)
8	VIAAT (SEQ ID NO: 59)	ATTTGGTTGTTTAGTGT (SEQ ID NO: 423)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
9	(SEQ ID NO: 1)	GTCGGTGGTTCGAGTA (SEQ ID NO: 424)
10	(SEQ ID NO: 1)	GTTGGTGGTTTGAGTAT (SEQ ID NO: 425)
11	(SEQ ID NO: 1)	GGAATTCGACGGGGAG (SEQ ID NO: 426)
12	(SEQ ID NO: 1)	GGGAATTTGATGGGGA (SEQ ID NO: 427)
13	(SEQ ID NO: 1)	TTCGTCGGGCGTTTAG (SEQ ID NO: 428)
14	(SEQ ID NO: 1)	TTTGTTGGGTGTTTAGT (SEQ ID NO: 429)
15	(SEQ ID NO: 1)	GTCGTTTCGTCGATGTA (SEQ ID NO: 430)
16	(SEQ ID NO: 1)	GGTTGTTTGTTGATGTAG (SEQ ID NO: 431)
17	(SEQ ID NO: 2)	GTATTGCGCGTTTATT (SEQ ID NO: 432)
18	(SEQ ID NO: 2)	AGGGTATTGTGTGTTTA (SEQ ID NO: 433)
19	(SEQ ID NO: 2)	AGGTACGTGGCGTTTT (SEQ ID NO: 434)
20	(SEQ ID NO: 2)	AGGTATGTGGTGTTTT (SEQ ID NO: 435)
21	(SEQ ID NO: 2)	GAGTTGCGCGGTAGTT (SEQ ID NO: 436)
22	(SEQ ID NO: 2)	AGGAGTTGTGTGGTAG (SEQ ID NO: 437)
23	(SEQ ID NO: 2)	ATAGTTTTCGCGTTTT (SEQ ID NO: 438)
24	(SEQ ID NO: 2)	AGTTTTTGTGTTT TAGGA (SEQ ID NO: 439)
25	(SEQ ID NO: 3)	TTTCGGTCCGGAATAT (SEQ ID NO: 440)
26	(SEQ ID NO: 3)	TTTGGTTGTGAATATTTT (SEQ ID NO: 441)
27	(SEQ ID NO: 3)	GTCGAGAGTTCGCGTT (SEQ ID NO: 442)
28	(SEQ ID NO: 3)	TAGTTGAGAGTTTGTGT (SEQ ID NO: 443)
29	(SEQ ID NO: 3)	TTTCGGTACGACGTTT (SEQ ID NO: 444)
30	(SEQ ID NO: 3)	GAGTTTTGGTATGATGT (SEQ ID NO: 445)
31	(SEQ ID NO: 3)	ATTGGGCGCGGTTTAA (SEQ ID NO: 446)
32	(SEQ ID NO: 3)	ATTGGGTGTGGTTTAA (SEQ ID NO: 447)
33	LIM/HOMEOBOX PROTEIN LHX9	ATTGTCGGGATACGTT (SEQ ID NO: 448)

No:	Gene	Oligo:
	(SEQ ID NO: 4)	
34	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	GATTGTTGGGATATGTT (SEQ ID NO: 449)
35	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	TTAGTGTCGCGTTATT (SEQ ID NO: 450)
36	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AGTGTTGTGTTATTTGG (SEQ ID NO: 451)
37	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	TGAAACGTTAGCGTTA (SEQ ID NO: 452)
38	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AGTGAAATGTTAGTGTT (SEQ ID NO: 453)
39	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	AAAGGCCGCGGTTTTTA (SEQ ID NO: 454)
40	LIM/HOMEBOX PROTEIN LHX9 (SEQ ID NO: 4)	TTGAAAGGTGTGGTTT (SEQ ID NO: 455)
41	(SEQ ID NO: 5)	TAAGTAGCGGCGTTGT (SEQ ID NO: 456)
42	(SEQ ID NO: 5)	TAAGTAGTGGTGTGTA (SEQ ID NO: 457)
43	(SEQ ID NO: 5)	GAGATGAGCGTCGTGG (SEQ ID NO: 458)
44	(SEQ ID NO: 5)	GAGATGAGTGTGTGG (SEQ ID NO: 459)
45	(SEQ ID NO: 5)	GTCGTTTCGTTAGTAACGG (SEQ ID NO: 460)
46	(SEQ ID NO: 5)	GTTGTTTGTAGTAATGG (SEQ ID NO: 461)
47	(SEQ ID NO: 5)	TATCGGTTTTTCGCGGT (SEQ ID NO: 462)
48	(SEQ ID NO: 5)	ATATTGGTTTTTGTGGT (SEQ ID NO: 463)
49	(SEQ ID NO: 5)	TTGGACGGCGTGTATT (SEQ ID NO: 464)
50	(SEQ ID NO: 5)	TTTGATGGTGTGTAT (SEQ ID NO: 465)
51	(SEQ ID NO: 6)	GACGTTGTCGTAATGA (SEQ ID NO: 466)
52	(SEQ ID NO: 6)	TGATGTTGTTGTAATGA (SEQ ID NO: 467)
53	(SEQ ID NO: 6)	AGTATACGAGACGCGA (SEQ ID NO: 468)
54	(SEQ ID NO: 6)	AGAGTATATGAGATGTGA (SEQ ID NO: 469)

No:	Gene	Oligo:
55	(SEQ ID NO: 6)	TTCGTTTATCGTGCGG (SEQ ID NO: 470)
56	(SEQ ID NO: 6)	TTTGTTTATTGTGTGGT (SEQ ID NO: 471)
57	(SEQ ID NO: 6)	AGGACGTAGAGCGTAG (SEQ ID NO: 472)
58	(SEQ ID NO: 6)	TGAGGATGTAGAGTGT (SEQ ID NO: 473)
59	(SEQ ID NO: 7)	TATAGACGGTGGGCGA (SEQ ID NO: 474)
60	(SEQ ID NO: 7)	TATAGATGGTGGGTGA (SEQ ID NO: 475)
61	(SEQ ID NO: 7)	ATTATCGCGGTGGTT (SEQ ID NO: 476)
62	(SEQ ID NO: 7)	GGATTATTGTGGTGG (SEQ ID NO: 477)
63	(SEQ ID NO: 7)	ATTCGTTGATTGCGGG (SEQ ID NO: 478)
64	(SEQ ID NO: 7)	TTTGTTGATTTGTGGGG (SEQ ID NO: 479)
65	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO- 1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TTTAGTCGATTGCGGA (SEQ ID NO: 480)
66	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-	AGTTGATTTGGGAGAA (SEQ ID NO: 481)

No:	Gene	Oligo:
	1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	
67	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO- 1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TGAGCGAGTTCGGAGA (SEQ ID NO: 482)
68	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO- 1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	GATGAGTGAGTTTGGA (SEQ ID NO: 483)
69	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN- HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE	TTTCGGGAGTTTCGTA (SEQ ID NO: 484)

No:	Gene	Oligo:
	PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	
70	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TTTGGGAGTTTTGTAGT (SEQ ID NO: 485)
71	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	TTTCGGTCGTCGTCGG (SEQ ID NO: 486)
72	UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR (UBIQUITIN-	ATTTTTGGTTGTAGTTGG (SEQ ID NO: 487)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO- 1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) (SEQ ID NO: 8)	
73	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTGAGTTCGGGTTCGT (SEQ ID NO: 488)
74	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTGAGTTTGGGTTTGT (SEQ ID NO: 489)
75	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TAGCGTATATGCGATT (SEQ ID NO: 490)
76	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGGTAGTGTATATGTGA (SEQ ID NO: 491)
77	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATATGCGATTGATTTTACGG (SEQ ID NO: 492)
78	BASSOON; ZINC	ATATGTGATTGATTTTATGG

No:	Gene	Oligo:
	FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	(SEQ ID NO: 493)
79	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTATAGCGTCGTATGG (SEQ ID NO: 494)
80	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATAGTGTTGTATGGGAA (SEQ ID NO: 495)
81	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GACGTAGGTTTCGTGAT (SEQ ID NO: 496)
82	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATGATGTAGGTTTGTGA (SEQ ID NO: 497)
83	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GGTAGCGTTTATTCGT (SEQ ID NO: 498)
84	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	AGGTAGTGTTTATTTGTA (SEQ ID NO: 499)
85	BASSOON; ZINC FINGER PROTEIN	ATAGTCGAGTTTCGTT (SEQ ID NO: 500)

No:	Gene	Oligo:
	231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	
86	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	GTTGAGTTTTGTTTAGG (SEQ ID NO: 501)
87	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TGGGTATACGTGTTAG (SEQ ID NO: 502)
88	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TATGGGTATATGTGTTAG (SEQ ID NO: 503)
89	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTAGATGCGTAAGGTT (SEQ ID NO: 504)
90	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	ATTAGATGTGTAAGGTTT (SEQ ID NO: 505)
91	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	TTATGGGTCGTAGGAT (SEQ ID NO: 506)
92	BASSOON; ZINC FINGER PROTEIN 231; NEURONAL	ATGGGTTGTAGGATTG (SEQ ID NO: 507)

No:	Gene	Oligo:
	DOUBLE ZINC FINGER PROTEIN (SEQ ID NO: 9)	
93	(SEQ ID NO: 10)	TTCGTTTAGTTACGTACGG (SEQ ID NO: 508)
94	(SEQ ID NO: 10)	TTTGTTTAGTTATGTATGG (SEQ ID NO: 509)
95	(SEQ ID NO: 10)	TAGTTACGTACGGATAT (SEQ ID NO: 510)
96	(SEQ ID NO: 10)	TTATGTATGGATATTTTGG (SEQ ID NO: 511)
97	(SEQ ID NO: 10)	AGGATACGTAGTTCGT (SEQ ID NO: 512)
98	(SEQ ID NO: 10)	AGGATATGTAGTTTGTATA (SEQ ID NO: 513)
99	(SEQ ID NO: 10)	AGTTCGTATATTTTCGG (SEQ ID NO: 514)
100	(SEQ ID NO: 10)	AGTTTGTATATTTTGGTA (SEQ ID NO: 515)
101	(SEQ ID NO: 11)	TACGGGGTCGTTTCGTA (SEQ ID NO: 516)
102	(SEQ ID NO: 11)	TATGGGGTTGTTTGTAT (SEQ ID NO: 517)
103	(SEQ ID NO: 11)	TTCGTAGGCGATCGTA (SEQ ID NO: 518)
104	(SEQ ID NO: 11)	GATTTGTAGGTGATTGT (SEQ ID NO: 519)
105	(SEQ ID NO: 11)	TAGCGGTCGATTTCGTT (SEQ ID NO: 520)
106	(SEQ ID NO: 11)	TAGTGGTTGATTGTTT (SEQ ID NO: 521)
107	(SEQ ID NO: 11)	GTCGTTACGTTTTTCGG (SEQ ID NO: 522)
108	(SEQ ID NO: 11)	TAGAGTTGTTATGTTTTTTGG (SEQ ID NO: 523)
109	(SEQ ID NO: 12)	AAGTTCGTTACGGCGG (SEQ ID NO: 524)
110	(SEQ ID NO: 12)	AGTTTGTATGGTGGG (SEQ ID NO: 525)
111	(SEQ ID NO: 12)	TACGTTGGTCGACGTT (SEQ ID NO: 526)
112	(SEQ ID NO: 12)	TTTATGTTGGTTGATGT (SEQ ID NO: 527)
113	(SEQ ID NO: 12)	GAGTCGGACGGTGTTT (SEQ ID NO: 528)
114	(SEQ ID NO: 12)	GAGTTGGATGGTGTTT (SEQ ID NO: 529)
115	HOOK2 PROTEIN	TAGCGTAAAGGGACGAG (SEQ ID NO: 530)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	(SEQ ID NO: 13)	
116	HOOK2 PROTEIN (SEQ ID NO: 13)	TAGTGTAAGGGATGAG (SEQ ID NO: 531)
117	HOOK2 PROTEIN (SEQ ID NO: 13)	ATGCGGATATTCGTT (SEQ ID NO: 532)
118	HOOK2 PROTEIN (SEQ ID NO: 13)	GGATGTGGATATTTTGT (SEQ ID NO: 533)
119	HOOK2 PROTEIN (SEQ ID NO: 13)	ATTCGTTTTTCGGAGT (SEQ ID NO: 534)
120	HOOK2 PROTEIN (SEQ ID NO: 13)	GGATATTTTGTGTTTGGGA (SEQ ID NO: 535)
121	HOOK2 PROTEIN (SEQ ID NO: 13)	AGGTAGCGTAAAGGGA (SEQ ID NO: 536)
122	HOOK2 PROTEIN (SEQ ID NO: 13)	AGGTAGTGTAAGGGA (SEQ ID NO: 537)
123	(SEQ ID NO: 14)	TAACGTATCGTTAGGG (SEQ ID NO: 538)
124	(SEQ ID NO: 14)	AATGTATTGTTAGGGATG (SEQ ID NO: 539)
125	(SEQ ID NO: 14)	TTTTGGCGCGGAGTA (SEQ ID NO: 540)
126	(SEQ ID NO: 14)	TTTGGTGTGGAGTAG (SEQ ID NO: 541)
127	(SEQ ID NO: 14)	TAGAGTTCGACGGGT (SEQ ID NO: 542)
128	(SEQ ID NO: 14)	AGAGTTTGATGGGTTT (SEQ ID NO: 543)
129	(SEQ ID NO: 14)	ATCGAATTATCGGTCGG (SEQ ID NO: 544)
130	(SEQ ID NO: 14)	ATTGAATTATTGGTTGG (SEQ ID NO: 545)
131	(SEQ ID NO: 14)	TATTACGGGGAACGGT (SEQ ID NO: 546)
132	(SEQ ID NO: 14)	TATTATGGGGAATGGTT (SEQ ID NO: 547)
133	(SEQ ID NO: 14)	GAACGGTTCGTTTTTA (SEQ ID NO: 548)
134	(SEQ ID NO: 14)	GGGAATGGTTTGTTTT (SEQ ID NO: 549)
135	(SEQ ID NO: 14)	AAGGGGATCGTTTTTT (SEQ ID NO: 550)
136	(SEQ ID NO: 14)	TAAGGGGATTGTTTTTT (SEQ ID NO: 551)

No:	Gene	Oligo:
137	(SEQ ID NO: 14)	TTTTAGGGCGGTTTAA (SEQ ID NO: 552)
138	(SEQ ID NO: 14)	TTAGGGTGGTTTAAGG (SEQ ID NO: 553)
139	(SEQ ID NO: 15)	TGACGAAAATCGATTG (SEQ ID NO: 554)
140	(SEQ ID NO: 15)	GATGAAAATTGATTGGAT (SEQ ID NO: 555)
141	(SEQ ID NO: 15)	GGGTATACGAATACGT (SEQ ID NO: 556)
142	(SEQ ID NO: 15)	GTGGGTATATGAATATGT (SEQ ID NO: 557)
143	(SEQ ID NO: 15)	TTCGAGGTTACGGGTT (SEQ ID NO: 558)
144	(SEQ ID NO: 15)	TTTGAGGTTATGGGTT (SEQ ID NO: 559)
145	(SEQ ID NO: 15)	TGTTTCGAGGTATATACGT (SEQ ID NO: 560)
146	(SEQ ID NO: 15)	TTGTTTGAGGTATATATGT (SEQ ID NO: 561)
147	(SEQ ID NO: 16)	AGGAGATTCGGTTATAT (SEQ ID NO: 562)
148	(SEQ ID NO: 16)	GAGGAGATTTGGTTATAT (SEQ ID NO: 563)
149	(SEQ ID NO: 16)	GTTATTTTCGGTAATGTT (SEQ ID NO: 564)
150	(SEQ ID NO: 16)	AGGTTATTTTGGAATG (SEQ ID NO: 565)
151	(SEQ ID NO: 16)	TATTAGTCGTTAGTTGA (SEQ ID NO: 566)
152	(SEQ ID NO: 16)	TATTAGTTGTTAGTTGAG (SEQ ID NO: 567)
153	(SEQ ID NO: 16)	AGGTTTATACGATAAAGG (SEQ ID NO: 568)
154	(SEQ ID NO: 16)	AGGTTTATATGATAAAGGT (SEQ ID NO: 569)
155	(SEQ ID NO: 17)	TTCGAATATTAGCGCGT (SEQ ID NO: 570)
156	(SEQ ID NO: 17)	ATTTTGAATATTAGTGTGT (SEQ ID NO: 571)
157	(SEQ ID NO: 17)	TTTATGAGCGGCGAGT (SEQ ID NO: 572)
158	(SEQ ID NO: 17)	GAGTGGTGAGTTTAGG (SEQ ID NO: 573)
159	(SEQ ID NO: 17)	AGTCGGTAACGCGTAT (SEQ ID NO: 574)
160	(SEQ ID NO: 17)	AGAGTTGGTAATGTGTA (SEQ ID NO: 575)
161	(SEQ ID NO: 17)	TTTTTTACGCGGAAGG (SEQ ID NO: 576)

No:	Gene	Oligo:
162	(SEQ ID NO: 17)	TTTTATGTGGAAGGGG (SEQ ID NO: 577)
163	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	AGGTCGGTCGTAGATA (SEQ ID NO: 578)
164	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	GAGGTTGGTTGTAGAT (SEQ ID NO: 579)
165	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	GACGTTTATTTTCGAGG (SEQ ID NO: 580)
166	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TGATGTTTATTTTGAGGT (SEQ ID NO: 581)
167	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE	TTTGATCGGGATGTGA (SEQ ID NO: 582)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	
168	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TTTGATTGGGATGTGA (SEQ ID NO: 583)
169	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	TGTAATTGACGTTTATTT (SEQ ID NO: 584)
170	LYSOSOMAL- ASSOCIATED MULTITRANSME MBRANE PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5 (SEQ ID NO: 18)	AATGTAATTGATGTTTATTT (SEQ ID NO: 585)
171	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATCGGTGTTAGCGGAT (SEQ ID NO: 586)
172	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE	AATTGGTGTTAGTGGA (SEQ ID NO: 587)

No:	Gene	Oligo:
	5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	
173	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATGTTTCGTAGGTGTCGG (SEQ ID NO: 588)
174	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	TTTGTAGGTGTTGGGTA (SEQ ID NO: 589)
175	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	GTCGTTGTTATCGAGG (SEQ ID NO: 590)
176	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	GGTTGTTGTTATTGAGG (SEQ ID NO: 591)
177	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATTGCGGTTTTATCGG (SEQ ID NO: 592)
178	"TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) (SEQ ID NO: 19)	ATTGTGGTTTTATTGGT (SEQ ID NO: 593)
179	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID)	TTCGATCGGTTGAATA (SEQ ID NO: 594)

No:	Gene	Oligo:
	EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	
180	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TTGAGTTTTGATTGGTT (SEQ ID NO: 595)
181	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAAGTCGCGTAAGGAG (SEQ ID NO: 596)
182	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AAGTTGTGTAAGGAGTA (SEQ ID NO: 597)
183	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGGTTCGTTAATCGTT (SEQ ID NO: 598)
184	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TGAGGTTTGTTAATTGT (SEQ ID NO: 599)

No:	Gene	Oligo:
185	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TACGTTGGACGTATAG (SEQ ID NO: 600)
186	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGAGTATGTTGGATGTA (SEQ ID NO: 601)
187	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTCGCGAGTTATCGA (SEQ ID NO: 602)
188	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTTGTGAGTTATTGAG (SEQ ID NO: 603)
189	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGCGCGTCGTATATA (SEQ ID NO: 604)
190	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR)	GGAGTAGTGTGTTGTAT (SEQ ID NO: 605)

No:	Gene	Oligo:
	(PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	
191	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GTCGAAAGTCGTTGAG (SEQ ID NO: 606)
192	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	GTTGAAAGTTGTTGAGG (SEQ ID NO: 607)
193	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGGACGTATCGCGAG (SEQ ID NO: 608)
194	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TAGGATGTATTGTGAGT (SEQ ID NO: 609)
195	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGTGTATCGTTTTTCGG (SEQ ID NO: 610)
196	PROSTAGLANDIN	TAGTGTATTGTTTTTTGG

No:	Gene	Oligo:
	E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	(SEQ ID NO: 611)
197	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TTCGTTTACGGTAGTT (SEQ ID NO: 612)
198	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	ATTTTGTATTATGGTAGTT (SEQ ID NO: 613)
199	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	TGCGTATCGTTAGTTA (SEQ ID NO: 614)
200	PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE (PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE) (SEQ ID NO: 20)	AGGTTGTGTATTGTTAG (SEQ ID NO: 615)
201	(SEQ ID NO: 21)	ATTCGGCGAATAGTAG (SEQ ID NO: 616)
202	(SEQ ID NO: 21)	TATTGGTGAATAGTAGTA (SEQ ID NO: 617)
203	(SEQ ID NO: 21)	ATAGCGTTGGTCGTTA (SEQ ID NO: 618)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
204	(SEQ ID NO: 21)	ATAGTGTGTTGGTTGTTAG (SEQ ID NO: 619)
205	(SEQ ID NO: 21)	TTCGGGATACGAGTTT (SEQ ID NO: 620)
206	(SEQ ID NO: 21)	GTTTGGGATATGAGTTT (SEQ ID NO: 621)
207	(SEQ ID NO: 21)	TACGATAAGTCGGAGA (SEQ ID NO: 622)
208	(SEQ ID NO: 21)	GGGTTATGATAAGTTGG (SEQ ID NO: 623)
209	(SEQ ID NO: 22)	TATCGGCGAGTTGTAT (SEQ ID NO: 624)
210	(SEQ ID NO: 22)	GGTTATTGGTGAGTTG (SEQ ID NO: 625)
211	(SEQ ID NO: 22)	TTAACGTTTGGGGACGT (SEQ ID NO: 626)
212	(SEQ ID NO: 22)	TTAATGTTTGGGGATGT (SEQ ID NO: 627)
213	(SEQ ID NO: 22)	TATTCGCGTTTTTAGAT (SEQ ID NO: 628)
214	(SEQ ID NO: 22)	TTATTTGTGTTTTTAGATTA (SEQ ID NO: 629)
215	EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE- SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR- SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	AGGGATAACGGAATATT (SEQ ID NO: 630)
216	EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE- SENSITIVE NUCLEOSIDE	GAAGGGATAATGGAATAT (SEQ ID NO: 631)

No:	Gene	Oligo:
	TRANSPORTER) (EQUILBRATIVE NBMPR- SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	
217	EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILBRATIVE NITROBENZYL MERCAPTOPYRIMIDINE RIBOSIDE- SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR- SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	GAATAGTTTCGAGATGA (SEQ ID NO: 632)
218	EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1 (EQUILBRATIVE NITROBENZYL MERCAPTOPYRIMIDINE RIBOSIDE- SENSITIVE NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR- SENSITIVE NUCLEOSIDE TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE (SEQ ID NO: 23)	GGAATAGTTTTGAGATGA (SEQ ID NO: 633)
219	ORPHAN NUCLEAR	TTTTCGACGAAGTTTT (SEQ ID NO: 634)

No:	Gene	Oligo:
	RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	
220	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TTTTGATGAAGTTTTGTT (SEQ ID NO: 635)
221	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TTACGGAGGCGTTTTA (SEQ ID NO: 636)
222	ORPHAN	TTTTATGGAGGTGTTTT

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	(SEQ ID NO: 637)
223	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	AGGCGAATTTATCGGG (SEQ ID NO: 638)
224	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	GGTGAATTTATTGGGG (SEQ ID NO: 639)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
225	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TAGTCGAAGTAGGCGT (SEQ ID NO: 640)
226	ORPHAN NUCLEAR RECEPTOR NR5A2 (ALPHA-1- FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION FACTOR) (B1- BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR) (SEQ ID NO: 24)	TAGTTGAAGTAGGTGTT (SEQ ID NO: 641)
227	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TTCGATCGAAGGTAAT (SEQ ID NO: 642)
228	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC	TTTGTGTTGATTGAAGGT (SEQ ID NO: 643)

No:	Gene	Oligo:
	3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	
229	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	AGGCGATCGATATTAG (SEQ ID NO: 644)
230	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	GGTGATTGATATTAGGG (SEQ ID NO: 645)
231	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	TTAGCGTTCGTCGTTA (SEQ ID NO: 646)
232	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL	TAATTAGTGTTTGTGTTA (SEQ ID NO: 647)

No:	Gene	Oligo:
	AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	
233	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	ATCGGTTCCGGAATTT (SEQ ID NO: 648)
234	PROTEIN- TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (IAR) (PHOGRIN) (SEQ ID NO: 25)	AGATTGGTTTGGGAAT (SEQ ID NO: 649)
235	(SEQ ID NO: 26)	GTCGATTTCGTTACGG (SEQ ID NO: 650)
236	(SEQ ID NO: 26)	GTTGATTTTGTATGGG (SEQ ID NO: 651)
237	(SEQ ID NO: 26)	TTCGGGTTTCGTATTA (SEQ ID NO: 652)
238	(SEQ ID NO: 26)	TTTTGGGTTTTGTATTAG (SEQ ID NO: 653)
239	(SEQ ID NO: 26)	AATTCGCGGTTTCGAT (SEQ ID NO: 654)
240	(SEQ ID NO: 26)	AATTTGTGGTTTGTATG (SEQ ID NO: 655)
241	(SEQ ID NO: 26)	GTCGTTTCGCGGAGAT (SEQ ID NO: 656)
242	(SEQ ID NO: 26)	GTTGTTTTGTGGAGATT (SEQ ID NO: 657)
243	(SEQ ID NO: 27)	ATTGGTCGATTCCGGG (SEQ ID NO: 658)
244	(SEQ ID NO: 27)	TATTGGTTGATTTGTGG (SEQ ID NO: 659)

No:	Gene	Oligo:
245	(SEQ ID NO: 27)	AGCGTTTCGATTTTCGG (SEQ ID NO: 660)
246	(SEQ ID NO: 27)	AGTGTTTTGATTTTGGT (SEQ ID NO: 661)
247	(SEQ ID NO: 27)	ATCGAGCGTTTCGATT (SEQ ID NO: 662)
248	(SEQ ID NO: 27)	GGATTGAGTGTTTTGAT (SEQ ID NO: 663)
249	(SEQ ID NO: 27)	ATTCGCGTATTCGAGA (SEQ ID NO: 664)
250	(SEQ ID NO: 27)	TTTGTGTATTTGAGAGG (SEQ ID NO: 665)
251	(SEQ ID NO: 27)	GACGTTTCGCGATTAAA (SEQ ID NO: 666)
252	(SEQ ID NO: 27)	TGGATGTTTGTGATTAA (SEQ ID NO: 667)
253	(SEQ ID NO: 27)	AAGTCGATATCGCGGT (SEQ ID NO: 668)
254	(SEQ ID NO: 27)	AAAAGTTGATATTGTGGT (SEQ ID NO: 669)
255	(SEQ ID NO: 27)	AGCGTTCGGAAGTTTA (SEQ ID NO: 670)
256	(SEQ ID NO: 27)	GGAGTGTTTGAAGTT (SEQ ID NO: 671)
257	(SEQ ID NO: 27)	TATTCGGACGGGGATA (SEQ ID NO: 672)
258	(SEQ ID NO: 27)	ATTTGGATGGGGATAG (SEQ ID NO: 673)
259	(SEQ ID NO: 27)	GAGACGCGTAGGTTAT (SEQ ID NO: 674)
260	(SEQ ID NO: 27)	GGGAGATGTGTAGGTT (SEQ ID NO: 675)
261	(SEQ ID NO: 28)	TAGTTTTTCGGCGAAGG (SEQ ID NO: 676)
262	(SEQ ID NO: 28)	GGTAGTTTTTGGTGAAG (SEQ ID NO: 677)
263	(SEQ ID NO: 28)	AAGGCGGTGACGTAAA (SEQ ID NO: 678)
264	(SEQ ID NO: 28)	AAGGTGGTGATGTAAA (SEQ ID NO: 679)
265	(SEQ ID NO: 28)	ATGGCGTAAGTACGTT (SEQ ID NO: 680)
266	(SEQ ID NO: 28)	GATGGTGTAAGTATGTT (SEQ ID NO: 681)
267	(SEQ ID NO: 28)	AGTACGTTCTGGGACGA (SEQ ID NO: 682)
268	(SEQ ID NO: 28)	AAGTATGTTTGGGATGA (SEQ ID NO: 683)
269	PEROXISOMAL MEMBRANE	ATGGTATTCGGGTCGT (SEQ ID NO: 684)

No:	Gene	Oligo:
	PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	
270	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TATGGTATTTGGGTTGT (SEQ ID NO: 685)
271	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TTGGAGCGTTAAGTAA (SEQ ID NO: 686)
272	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TATTTGGAGTGTTAAGTA (SEQ ID NO: 687)
273	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14)	TGAAAGATTCGTTTGT (SEQ ID NO: 688)

No:	Gene	Oligo:
	(PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	
274	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	GTGAAAGATTTGTTTGT (SEQ ID NO: 689)
275	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TGTATAACGAGAGGTG (SEQ ID NO: 690)
276	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	TGTATAATGAGAGGTGA (SEQ ID NO: 691)
277	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE	ATGTTTCGGGTATGGA (SEQ ID NO: 692)

No:	Gene	Oligo:
	ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	
278	PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING PROTEIN) (SEQ ID NO: 29)	ATGTTTTGGGTATGGA (SEQ ID NO: 693)
279	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	TTTTCGAGGAATTCGT (SEQ ID NO: 694)
280	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	TTTTTTGAGGAATTTGTT (SEQ ID NO: 695)
281	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	ATAGTTTTTCGGCGGGT (SEQ ID NO: 696)
282	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	TATAGTTTTTGGTGGGT (SEQ ID NO: 697)
283	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	TTTTTCGGCGTAGATA (SEQ ID NO: 698)
284	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX- 2.2) (SEQ ID NO: 30)	TGTTTTTTGGTGTAGAT (SEQ ID NO: 699)
285	HOMEBOX PROTEIN HOX-B6	TTACGGGCGTTAGAGA (SEQ ID NO: 700)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	(HOX-2B) (HOX-2.2) (SEQ ID NO: 30)	
286	HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (SEQ ID NO: 30)	GGAGTTATGGGTGTTA (SEQ ID NO: 701)
287	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	TATCGGATTATCGCGG (SEQ ID NO: 702)
288	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	ATTGGATTATTGTGGGG (SEQ ID NO: 703)
289	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	GTCGGTAGTTTATCGGAT (SEQ ID NO: 704)
290	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	GTTGGTAGTTTATTGGAT (SEQ ID NO: 705)
291	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	TAGGAGACGTTACGTT (SEQ ID NO: 706)
292	LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1) (SEQ ID NO: 31)	AGATGTTATGTTAGGGT (SEQ ID NO: 707)
293	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)	AAGAACGGACGTGTTT (SEQ ID NO: 708)

No:	Gene	Oligo:
	(SEQ ID NO: 32)	
294	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	AGGAAGAATGGATGTG (SEQ ID NO: 709)
295	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TTTTTGCGATAGTCGG (SEQ ID NO: 710)
296	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	GTTTTTGTGATAGTTGG (SEQ ID NO: 711)
297	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA-	TAGCGGCGATTTAAGG (SEQ ID NO: 712)

No:	Gene	Oligo:
	RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	
298	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	GTAGTGGTGATTTAAGG (SEQ ID NO: 713)
299	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TTTACGAGCGAGTCGT (SEQ ID NO: 714)
300	LOW AFFINITY IMMUNOGLOBULIN IN GAMMA FC REGION RECEPTOR II-A PRECURSOR (FC- GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR II-A) (FC-GAMMA- RIIA) (CD32) (CDW32) (SEQ ID NO: 32)	TTTTATGAGTGAGTTGTT (SEQ ID NO: 715)
301	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT	TTTCGATAGTATACGGG (SEQ ID NO: 716)

No:	Gene	Oligo:
	3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER ASE 3) (SEQ ID NO: 33)	
302	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT 3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER ASE 3) (SEQ ID NO: 33)	TTTGATAGTATATGGGGA (SEQ ID NO: 717)
303	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT 3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER	AAGGGAGCGTTCGTTA (SEQ ID NO: 718)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	ASE 3) (SEQ ID NO: 33)	
304	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT 3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER ASE 3) (SEQ ID NO: 33)	AAGGGAGTGTTTGTTA (SEQ ID NO: 719)
305	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT 3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER ASE 3) (SEQ ID NO: 33)	AATAATAGCGACGGGG (SEQ ID NO: 720)
306	1-ACYL-SN- GLYCEROL-3- PHOSPHATE ACYLTRANSFER ASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFER ASE 3) (1-AGPAT	TAATAGTGATGGGGGT (SEQ ID NO: 721)

No:	Gene	Oligo:
	3) (LYSOPHOSPHAT IDIC ACID ACYLTRANSFER ASE-GAMMA) (LPAAT-GAMMA) (1- ACYLGLYCEROL- 3-PHOSPHATE O- ACYLTRANSFER ASE 3) (SEQ ID NO: 33)	
307	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTAGAATCGTCGAGT (SEQ ID NO: 722)
308	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	AGAATTGTTGAGTGAAG (SEQ ID NO: 723)
309	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTTTCGTCGGTTCGTA (SEQ ID NO: 724)
310	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTGTTGGTTTGTAGGA (SEQ ID NO: 725)
311	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	AGGACGGCGTTTATTA (SEQ ID NO: 726)
312	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	GATGAGGATGGTGTTT (SEQ ID NO: 727)
313	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTCGATTTCGGAGGAT (SEQ ID NO: 728)
314	HOMEBOX PROTEIN GSH-2 (SEQ ID NO: 34)	TTTGATTTTGGAGGATT (SEQ ID NO: 729)
315	(SEQ ID NO: 35)	TTCGTTATCGAGAGTT (SEQ ID NO: 730)
316	(SEQ ID NO: 35)	GGGTTTGTATTGAGA (SEQ ID NO: 731)
317	(SEQ ID NO: 35)	GACGTGAGCGTTTAGG (SEQ ID NO: 732)

No:	Gene	Oligo:
318	(SEQ ID NO: 35)	GATGTGAGTGTTTAGGG (SEQ ID NO: 733)
319	(SEQ ID NO: 35)	TACGGAGTTGGCGTTA (SEQ ID NO: 734)
320	(SEQ ID NO: 35)	TTTATGGAGTTGGTGT (SEQ ID NO: 735)
321	(SEQ ID NO: 35)	TTGGTTCGTCGAGGAT (SEQ ID NO: 736)
322	(SEQ ID NO: 35)	TTGGTTTGTGAGGAT (SEQ ID NO: 737)
323	HISTONE H4 (SEQ ID NO: 36)	ATCGAAATCGTAGAGG (SEQ ID NO: 738)
324	HISTONE H4 (SEQ ID NO: 36)	ATTGAAATTGTAGAGGG (SEQ ID NO: 739)
325	HISTONE H4 (SEQ ID NO: 36)	TATGGCGGTGATCGTT (SEQ ID NO: 740)
326	HISTONE H4 (SEQ ID NO: 36)	TTTATGGTGGTGATTGT (SEQ ID NO: 741)
327	HISTONE H4 (SEQ ID NO: 36)	TTACGGCGTTTCGGAT (SEQ ID NO: 742)
328	HISTONE H4 (SEQ ID NO: 36)	TTATGGTGTGTTTGGATT (SEQ ID NO: 743)
329	HISTONE H4 (SEQ ID NO: 36)	ATGCGTTTTACGTCGT (SEQ ID NO: 744)
330	HISTONE H4 (SEQ ID NO: 36)	AGATGTGTTTTATGTTGT (SEQ ID NO: 745)
331	HISTONE H4 (SEQ ID NO: 36)	TAAGGCGTCGGATGGT (SEQ ID NO: 746)
332	HISTONE H4 (SEQ ID NO: 36)	GAGTAAGGTGTTGGAT (SEQ ID NO: 747)
333	HISTONE H4 (SEQ ID NO: 36)	TATTTTACGGTGGCGT (SEQ ID NO: 748)
334	HISTONE H4 (SEQ ID NO: 36)	ATTTTATGGTGGTGTGTT (SEQ ID NO: 749)
335	POTASSIUM VOLTAGE- GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTO MA- SPECIFIC POTASSIUM CHANNEL KQT- LIKE 2) (SEQ ID NO: 37)	ATTCGGAGGTATCGT (SEQ ID NO: 750)
336	POTASSIUM VOLTAGE- GATED CHANNEL SUBFAMILY KQT MEMBER 2	TTTGGAGGTATTGTGT (SEQ ID NO: 751)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	(NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	
337	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TTCGTACGGGGTATAG (SEQ ID NO: 752)
338	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	GGTTTGTATGGGGTATA (SEQ ID NO: 753)
339	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	TATAAGGCGTTACGGT (SEQ ID NO: 754)
340	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2) (SEQ ID NO: 37)	GGTATAAGGTGTTATGG (SEQ ID NO: 755)

No:	Gene	Oligo:
341	POTASSIUM VOLTAGE- GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTO MA- SPECIFIC POTASSIUM CHANNEL KQT- LIKE 2) (SEQ ID NO: 37)	TTACGGTCGCGTAGTA (SEQ ID NO: 756)
342	POTASSIUM VOLTAGE- GATED CHANNEL SUBFAMILY KQT MEMBER 2 (NEUROBLASTO MA- SPECIFIC POTASSIUM CHANNEL KQT- LIKE 2) (SEQ ID NO: 37)	TATGGTTGTGTAGTAGT (SEQ ID NO: 757)
343	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	TTATTCGTAGTTTTTCGG (SEQ ID NO: 758)
344	ADAPTER-	GTTTATTTGTAGTTTTTGG

No:	Gene	Oligo:
	RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/API ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	(SEQ ID NO: 759)
345	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/API ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1	TGTAATCGTTTATTCGT (SEQ ID NO: 760)

No:	Gene	Oligo:
	CLATHRIN) (DC22) (SEQ ID NO: 38)	
346	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	TAATTGTTTATTTGTAGTTT (SEQ ID NO: 761)
347	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1	TTCGAAGTCGGGATTA (SEQ ID NO: 762)

No:	Gene	Oligo:
	SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	
348	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	ATTTTGAAGTTGGGATT (SEQ ID NO: 763)
349	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT)	ATCGAGAGTATTTCGAAG (SEQ ID NO: 764)

No:	Gene	Oligo:
	(CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	
350	ADAPTER- RELATED PROTEIN COMPLEX 1 SIGMA 1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA- 1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22) (SEQ ID NO: 38)	GGATTGAGAGTATTTTGA (SEQ ID NO: 765)
351	(SEQ ID NO: 39)	TAAGCGGTATAAGTCGG (SEQ ID NO: 766)
352	(SEQ ID NO: 39)	AGTGGTATAAGTTGGTT (SEQ ID NO: 767)
353	(SEQ ID NO: 39)	TTCGGTAAGCGGTATA (SEQ ID NO: 768)
354	(SEQ ID NO: 39)	ATAATTTGGTAAGTGGTA (SEQ ID NO: 769)
355	(SEQ ID NO: 39)	TTCGTGATTTTACGTTA (SEQ ID NO: 770)
356	(SEQ ID NO: 39)	AATTTTGTGATTTTATGTT (SEQ ID NO: 771)

No:	Gene	Oligo:
357	(SEQ ID NO: 39)	TGGCGACGAAGTGTA (SEQ ID NO: 772)
358	(SEQ ID NO: 39)	TTTGTGGTGATGAAGT (SEQ ID NO: 773)
359	(SEQ ID NO: 40)	TAGCGGGTTTACGGAG (SEQ ID NO: 774)
360	(SEQ ID NO: 40)	AGTAGTGGGTTTATGG (SEQ ID NO: 775)
361	(SEQ ID NO: 40)	TAACGAGTCGAGCGGA (SEQ ID NO: 776)
362	(SEQ ID NO: 40)	AATGAGTTGAGTGGAG (SEQ ID NO: 777)
363	(SEQ ID NO: 40)	TTTTCGCGTGTAAGTT (SEQ ID NO: 778)
364	(SEQ ID NO: 40)	TTTTTGTGTGTAAGTTAA (SEQ ID NO: 779)
365	(SEQ ID NO: 40)	TAGGACGATTCCGATA (SEQ ID NO: 780)
366	(SEQ ID NO: 40)	AGGATGATTTGGATAGT (SEQ ID NO: 781)
367	(SEQ ID NO: 40)	TTCGAGTGAAAGCGGTA (SEQ ID NO: 782)
368	(SEQ ID NO: 40)	TTTGAGTGAAAGTGGTA (SEQ ID NO: 783)
369	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTACGTTTTCGTGAAAT (SEQ ID NO: 784)
370	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTTTATGTTTTTGTGAAAT (SEQ ID NO: 785)
371	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN)	GGGAGGACGTAGAGTA (SEQ ID NO: 786)

No:	Gene	Oligo:
	(SEQ ID NO: 41)	
372	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	GGGAGGATGTAGAGTA (SEQ ID NO: 787)
373	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGGTTATCGTTTATATT (SEQ ID NO: 788)
374	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TTGGGTTATTGTTTATATT (SEQ ID NO: 789)
375	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGTATCGGTTTTTGAA (SEQ ID NO: 790)
376	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTI C PEMPHIGUS ANTIGEN) (SEQ ID NO: 41)	TGGTATTGGTTTTTGAA (SEQ ID NO: 791)
377	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190	GTTTAGGTTTCGAGTTTA (SEQ ID NO: 792)

No:	Gene	Oligo:
	KDA PARANEOPLASTIC PEMPFIGUS ANTIGEN) (SEQ ID NO: 41)	
378	PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC PEMPFIGUS ANTIGEN) (SEQ ID NO: 41)	GGTTTAGGTTTGAGTTTA (SEQ ID NO: 793)
379	(SEQ ID NO: 42)	AGAATTGCGACGGTTT (SEQ ID NO: 794)
380	(SEQ ID NO: 42)	AATTGTGATGGTTTGTA (SEQ ID NO: 795)
381	(SEQ ID NO: 42)	TTACGTTTATTTACGGG (SEQ ID NO: 796)
382	(SEQ ID NO: 42)	TATGTTTATTTATGGGGAT (SEQ ID NO: 797)
383	(SEQ ID NO: 42)	TGGATGTGCGGAAGAA (SEQ ID NO: 798)
384	(SEQ ID NO: 42)	GATGTGTGGAAGAAGT (SEQ ID NO: 799)
385	(SEQ ID NO: 42)	ATGGGTACGTTGTTTA (SEQ ID NO: 800)
386	(SEQ ID NO: 42)	TATGGGTATGTTGTTTAT (SEQ ID NO: 801)
387	(SEQ ID NO: 42)	GGATATTTGCGTTAGTA (SEQ ID NO: 802)
388	(SEQ ID NO: 42)	GGATATTTGTGTTAGTATT (SEQ ID NO: 803)
389	(SEQ ID NO: 43)	GACGTGTTTCGGGTTTAA (SEQ ID NO: 804)
390	(SEQ ID NO: 43)	GATGTGTTTGGGTTTAA (SEQ ID NO: 805)
391	(SEQ ID NO: 43)	AGTCGACGGTTTGAGG (SEQ ID NO: 806)
392	(SEQ ID NO: 43)	AGTTGATGGTTTGAGG (SEQ ID NO: 807)
393	(SEQ ID NO: 43)	TTATTGCGTTGTAAAGT (SEQ ID NO: 808)
394	(SEQ ID NO: 43)	GTTATTGTGTTGTAAAGT (SEQ ID NO: 809)
395	(SEQ ID NO: 44)	ATTAAACGGGGTCGT (SEQ ID NO: 810)
396	(SEQ ID NO: 44)	AATTAAATGGGGTTGT (SEQ ID NO: 811)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
397	(SEQ ID NO: 44)	ATCGGTTTTTTGTATCGAATA (SEQ ID NO: 812)
398	(SEQ ID NO: 44)	ATTGGTTTTTTGTATTGAATA (SEQ ID NO: 813)
399	(SEQ ID NO: 44)	TTCGGCGTTTTTCGTAG (SEQ ID NO: 814)
400	(SEQ ID NO: 44)	TGAAAGTTCGGCGTTT (SEQ ID NO: 815)
401	(SEQ ID NO: 44)	TTTGGTGTTTTTGTAGG (SEQ ID NO: 816)
402	(SEQ ID NO: 44)	TGAAAGTTTGGTGTTTT (SEQ ID NO: 817)
403	(SEQ ID NO: 45)	ATCGGTTTTTCGAGGT (SEQ ID NO: 818)
404	(SEQ ID NO: 45)	ATTGGTTTTTTGAGGTT (SEQ ID NO: 819)
405	(SEQ ID NO: 45)	GGTCGATTTTCGCGTA (SEQ ID NO: 820)
406	(SEQ ID NO: 45)	TGGTTGATTTTGTGTA (SEQ ID NO: 821)
407	(SEQ ID NO: 46)	GGTAATTCGCGTATT (SEQ ID NO: 822)
408	(SEQ ID NO: 46)	TTGGTAATTTTGTGTATT (SEQ ID NO: 823)
409	(SEQ ID NO: 47)	TATGCGTATACGTGGT (SEQ ID NO: 824)
410	(SEQ ID NO: 47)	ATGTGTATATGTGGTTTT (SEQ ID NO: 825)
411	(SEQ ID NO: 47)	GTCGTTTTATGCGTAT (SEQ ID NO: 826)
412	(SEQ ID NO: 47)	TGGTTGTTTTATGTGTAT (SEQ ID NO: 827)
413	(SEQ ID NO: 47)	TAGTTTTCGAATTCGT (SEQ ID NO: 828)
414	(SEQ ID NO: 47)	ATTAGTTTTTGAATTTTGT (SEQ ID NO: 829)
415	(SEQ ID NO: 48)	TAGCGAGGGTCGTTTT (SEQ ID NO: 830)
416	(SEQ ID NO: 48)	TAGTGAGGGTTGTTTT (SEQ ID NO: 831)
417	(SEQ ID NO: 48)	TTAGGTCGCGTCGGTA (SEQ ID NO: 832)
418	(SEQ ID NO: 48)	AGGTTGTGTTGGTAGA (SEQ ID NO: 833)
419	(SEQ ID NO: 48)	ATTTCGTTTACGTCGT (SEQ ID NO: 834)
420	(SEQ ID NO: 48)	GGATTTTGTTTATGTTGT (SEQ ID NO: 835)
421	(SEQ ID NO: 48)	TTTTCGTATTCGGGTA (SEQ ID NO: 836)

No:	Gene	Oligo:
422	(SEQ ID NO: 48)	TTTGTATTGGGTAAAAG (SEQ ID NO: 837)
423	(SEQ ID NO: 48)	AGGATCGGGATTTCGTA (SEQ ID NO: 838)
424	(SEQ ID NO: 48)	AGGATTGGGATTTGTAG (SEQ ID NO: 839)
425	(SEQ ID NO: 48)	TTCGTTTAAGCGGGGT (SEQ ID NO: 840)
426	(SEQ ID NO: 48)	TTTGTTTAAGTGGGGT (SEQ ID NO: 841)
427	(SEQ ID NO: 49)	ATATTCGTGCGGTCGG (SEQ ID NO: 842)
428	(SEQ ID NO: 49)	ATATTTGTGTGGTTGGA (SEQ ID NO: 843)
429	(SEQ ID NO: 49)	TTAGGTCGTGGAATGT (SEQ ID NO: 844)
430	(SEQ ID NO: 49)	TTAGGTTGTGGAATGT (SEQ ID NO: 845)
431	(SEQ ID NO: 49)	AGGAATCGTGAGTAGG (SEQ ID NO: 846)
432	(SEQ ID NO: 49)	AGGAATTGTGAGTAGG (SEQ ID NO: 847)
433	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTCGATATCGAGTCGG (SEQ ID NO: 848)
434	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	ATTTGATATTGAGTTGGT (SEQ ID NO: 849)
435	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	ATTCGCGTTTAAACGT (SEQ ID NO: 850)
436	DNA REPLICATION FACTOR; DOUBLE	TTTGTGTTTAAATGTGGA (SEQ ID NO: 851)

No:	Gene	Oligo:
	PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	
437	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTCGGTTGGGACGTAA (SEQ ID NO: 852)
438	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTTGGTTGGGATGTAA (SEQ ID NO: 853)
439	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTAAGGCGTTTAGCGA (SEQ ID NO: 854)
440	DNA REPLICATION FACTOR; DOUBLE PARKED, DROSOPHILA, HOMOLOG OF (SEQ ID NO: 50)	TTTTAAGGTGTTTAGTGA (SEQ ID NO: 855)
441	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TATCGTCGAGTGTGTA (SEQ ID NO: 856)
442	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	GGGGTTATTGTTGAGT (SEQ ID NO: 857)
443	PR-DOMAIN ZINC FINGER PROTEIN	TATTATTCGAGTTAGAGG (SEQ ID NO: 858)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	
444	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TTATTATTTGAGTTAGAGG (SEQ ID NO: 859)
445	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	AGGATTCGTTGAAGAA (SEQ ID NO: 860)
446	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	GTAGGATTTGTTGAAGA (SEQ ID NO: 861)
447	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TTATTAGGCGATATTTTAA (SEQ ID NO: 862)
448	PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1) (SEQ ID NO: 51)	TATTAGGTGATATTTTAAGT (SEQ ID NO: 863)
449	TUMOR SUPPRESSING SUBTRANSFERA BLE CANDIDATE 5; P45 BECKWITH- WIEDEMANN REGION 1A; BECKWITH- WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-	TAGTACGTTGGTTCGG (SEQ ID NO: 864)

No:	Gene	Oligo:
	LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER- RELATED PROTEIN (SEQ ID NO: 52)	
450	TUMOR SUPPRESSING SUBTRANSFERA BLE CANDIDATE 5; P45 BECKWITH- WIEDEMANN REGION 1A; BECKWITH- WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER- LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER- RELATED PROTEIN (SEQ ID NO: 52)	TATGTTGGTTTGGAGT (SEQ ID NO: 865)
451	TUMOR SUPPRESSING	AGTTGTTTCGATGATTAG (SEQ ID NO: 866)

No:	Gene	Oligo:
	SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
452	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-	TTTAGTTGTTTGATGATTA (SEQ ID NO: 867)

No:	Gene	Oligo:
	LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
453	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	AGATTAGTACGTTGGTT (SEQ ID NO: 868)
454	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-	AAGATTAGTATGTTGGTT (SEQ ID NO: 869)

No:	Gene	Oligo:
	WIEDEMANN REGION 1A; BECKWITH- WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER- LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER- RELATED PROTEIN (SEQ ID NO: 52)	
455	TUMOR SUPPRESSING SUBTRANSFERA BLE CANDIDATE 5; P45 BECKWITH- WIEDEMANN REGION 1A; BECKWITH- WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER- LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED	TTAAAGCGGGGAGTTT (SEQ ID NO: 870)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
456	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	GTTTAAAGTGGGGAGT (SEQ ID NO: 871)
457	TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN	AGATGGTATCGTTTAGG (SEQ ID NO: 872)

No:	Gene	Oligo:
	SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER- LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER- RELATED PROTEIN (SEQ ID NO: 52)	
458	TUMOR SUPPRESSING SUBTRANSFERA BLE CANDIDATE 5; P45 BECKWITH- WIEDEMANN REGION 1A; BECKWITH- WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER- LIKE PROTEIN; ORGANIC CATION TRANSPORTER- LIKE 2; TUMOR- SUPPRESSING STF CDNA 5; IMPRINTED MULTI- MEMBRANE SPANNING POLYSPECIFIC	ATGGTATTGTTTAGGTG (SEQ ID NO: 873)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
	TRANSPORTER-RELATED PROTEIN (SEQ ID NO: 52)	
459	CDH1 (SEQ ID NO: 54)	TATCGCGTTTATGCGA (SEQ ID NO: 874)
460	CDH1 (SEQ ID NO: 54)	ATTGTGTTTATGTGAGG (SEQ ID NO: 875)
461	CDH1 (SEQ ID NO: 54)	TTATGCGAGGTCGGGT (SEQ ID NO: 876)
462	CDH1 (SEQ ID NO: 54)	TTATGTGAGGTTGGGT (SEQ ID NO: 877)
463	CDH1 (SEQ ID NO: 54)	TTAATTAGCGGTACGG (SEQ ID NO: 878)
464	CDH1 (SEQ ID NO: 54)	AATTAGTGGTATGGGG (SEQ ID NO: 879)
465	CDH1 (SEQ ID NO: 54)	TAGTGGCGTCGGAATT (SEQ ID NO: 880)
466	CDH1 (SEQ ID NO: 54)	TAGTGGTGTGGAATT (SEQ ID NO: 881)
467	CDKN2a (SEQ ID NO: 55)	GGCGTTGTTTAACGTAT (SEQ ID NO: 882)
468	CDKN2a (SEQ ID NO: 55)	GGGTGTTGTTTAATGTA (SEQ ID NO: 883)
469	CDKN2a (SEQ ID NO: 55)	TGTTTAACGTATCGAAT (SEQ ID NO: 884)
470	CDKN2a (SEQ ID NO: 55)	GTTGTTTAATGTATTGAAT (SEQ ID NO: 885)
471	CDKN2a (SEQ ID NO: 55)	AATAGTTACGGTCGGA (SEQ ID NO: 886)
472	CDKN2a (SEQ ID NO: 55)	AGTTATGGTTGGAGGT (SEQ ID NO: 887)
473	CDKN2a (SEQ ID NO: 55)	GTCGGAGGTCGATTTA (SEQ ID NO: 888)
474	CDKN2a (SEQ ID NO: 55)	GGTTGGAGGTTGATTTA (SEQ ID NO: 889)
475	CD44 (SEQ ID NO: 56)	AGGTATTTTCGCGATAT (SEQ ID NO: 890)
476	CD44 (SEQ ID NO: 56)	AGGTATTTTGTGATATTTT (SEQ ID NO: 891)
477	CD44 (SEQ ID NO: 56)	TAGGTTTCGGTTCGTTAT (SEQ ID NO: 892)
478	CD44 (SEQ ID NO: 56)	TAGGTTTGGTTTGTATT (SEQ ID NO: 893)
479	CD44 (SEQ ID NO: 56)	GTTCGTTTCGGATATTA (SEQ ID NO: 894)
480	CD44 (SEQ ID NO: 56)	TTTGTTTGGATATTATGG (SEQ ID NO: 895)
481	CD44 (SEQ ID NO: 56)	TTTGGCGTAGATCGGT (SEQ ID NO: 896)

No:	Gene	Oligo:
482	CD44 (SEQ ID NO: 56)	TTTGGTGTAGATTGGT (SEQ ID NO: 897)
483	CD44 (SEQ ID NO: 56)	TTTAGCGCGGATTCGG (SEQ ID NO: 898)
484	CD44 (SEQ ID NO: 56)	GTTTAGTGTGGATTGG (SEQ ID NO: 899)
485	GSTP1 (SEQ ID NO: 57)	ATCGTTGCGATTTCGG (SEQ ID NO: 900)
486	GSTP1 (SEQ ID NO: 57)	ATTGTTGTGATTTTGA (SEQ ID NO: 901)
487	GSTP1 (SEQ ID NO: 57)	AGTGTGCGTAGCGAAT (SEQ ID NO: 902)
488	GSTP1 (SEQ ID NO: 57)	GTGTGTAGTGAATTGG (SEQ ID NO: 903)
489	GSTP1 (SEQ ID NO: 57)	GAGTCGTCGCGTAGTT (SEQ ID NO: 904)
490	GSTP1 (SEQ ID NO: 57)	GGAGTTGTTGTGTAGTT (SEQ ID NO: 905)
491	GSTP1 (SEQ ID NO: 57)	ATTTTCGTCGGTTTTAG (SEQ ID NO: 906)
492	GSTP1 (SEQ ID NO: 57)	GGATTTTGTGTTGGTTTA (SEQ ID NO: 907)
493	GSTP1 (SEQ ID NO: 57)	TTCGCGGTTTTCGAGT (SEQ ID NO: 908)
494	GSTP1 (SEQ ID NO: 57)	TTTGTGGTTTTTGAGTT (SEQ ID NO: 909)
495	GSTP1 (SEQ ID NO: 57)	TAGCGAAGTTTCGCGG (SEQ ID NO: 910)
496	GSTP1 (SEQ ID NO: 57)	AGTGAAGTTTTGTGGT (SEQ ID NO: 911)
497	GSTP1 (SEQ ID NO: 57)	GTCGCGCGTATTTATT (SEQ ID NO: 912)
498	GSTP1 (SEQ ID NO: 57)	GGGTTGTGTGATTTAT (SEQ ID NO: 913)
499	IGF2 (SEQ ID NO: 58)	TACGTATAAAATTCGTATT (SEQ ID NO: 914)
500	IGF2 (SEQ ID NO: 58)	AAATTATGTATAAAATTTGT (SEQ ID NO: 915)
501	IGF2 (SEQ ID NO: 58)	ATAGACGCGAGTTCGG (SEQ ID NO: 916)
502	IGF2 (SEQ ID NO: 58)	AGATGTGAGTTTGGTT (SEQ ID NO: 917)
503	IGF2 (SEQ ID NO: 58)	TATCGGGGTGCGTTTA (SEQ ID NO: 918)
504	IGF2 (SEQ ID NO: 58)	ATTGGGGTGTGTTTAA (SEQ ID NO: 919)
505	IGF2 (SEQ ID NO: 58)	TTACGGAGGTTTCGGT (SEQ ID NO: 920)
506	IGF2 (SEQ ID NO: 58)	TTATGGAGGTTTTGGT (SEQ ID NO: 921)

<i>No:</i>	<i>Gene</i>	<i>Oligo:</i>
507	AR (SEQ ID NO: 53)	TTATAGTCGTAAGTCGGT (SEQ ID NO: 922)
508	AR (SEQ ID NO: 53)	AGTTGTAGTTGGTTTTG (SEQ ID NO: 923)
509	AR (SEQ ID NO: 53)	GTCGTGGTCGTTAGTA (SEQ ID NO: 924)
510	AR (SEQ ID NO: 53)	GTTGTGGTTGTTAGTAA (SEQ ID NO: 925)
511	AR (SEQ ID NO: 53)	TATTTTCGGACGAGGA (SEQ ID NO: 926)
512	AR (SEQ ID NO: 53)	AGTATTTTGGATGAGG (SEQ ID NO: 927)

Example 4:

In the following analysis the methylation status of the genes according to Table 10 were analysed by means of methylation specific polymerase chain reaction using the primers according to Table 10 (below).

The study was run on 50 prostate cancer and 50 Benign Prostate Hyperplasia (BPH) tissue samples. Genomic DNA was analyzed using the MSP technique after bisulfite conversion. The bisulfite process converts unmethylated cytosines to uracil while methylated cytosines remained conserved. Bisulfite treatment was performed with minor modifications according to the protocol described in Olek et al. (1996). Sequences of interest were then amplified by means of methylation specific primers, and the amplificate is detected by means of Taqman probes (see Table 10).

Table 10

Genomic SEQ ID NO:	Primer	Primer	Taqman probe
20	Cgcgctactccgcataca (SEQ ID NO: 958)	Gaggtaatcgaggcggtcg (SEQ ID NO: 959)	56-FAM/cgccaattcatagccgcacc/3BHQ (SEQ ID NO: 960)
36	Accgaaaatacgcttcacg (SEQ ID NO: 961)	Gcggtatcgtaaagtattgcgc (SEQ ID NO: 962)	/56-FAM/cgcgacgaacaaaacgccg/3BHQ_1/ (SEQ ID NO: 963)
36	Gcggtttacgctgctgcg (SEQ ID NO: 964)	Gacgctaaacgccaccgt (SEQ ID NO: 965)	/56-FAM/ccgaccatccgacgccttactcg/3BHQ_1/ (SEQ ID NO: 966)
51	Cgaatttataccgaacgctcctacg (SEQ ID NO: 967)	Aggttacgggaggctcgaggtcg (SEQ ID NO: 968)	56-FAM/ cccgcctatcaccgttcccgaaccctta/3BHQ (SEQ

			ID NO: 969)
51	Tcccgaattataccgaacg (SEQ ID NO: 970)	Ttttatttaggggtcggaac (SEQ ID NO: 971)	56-FAM/ acgccccgccatcgaccg/3BHQ_1 (SEQ ID NO: 972)
24	Ttgtggttcgggaagagac (SEQ ID NO: 973)	Cttcgatcgaaaaaacccg (SEQ ID NO: 974)	56-FAM/ aactacgcgcaaaccgcga/3BHQ (SEQ ID NO: 975)
31	Cgttttcgtttatttcgc (SEQ ID NO: 976)	Gacaaaaaacgccacgtc (SEQ ID NO: 977)	56-FAM/ccgacaattcaccgaatcaccg/3BHQ_1 (SEQ ID NO: 978)
11	Attcacctaccgtcgcg (SEQ ID NO: 979)	Taggagtgcgatcgtttc (SEQ ID NO: 980)	56-FAM/acgaacggttacgaccgatacccaacta/3BHQ (SEQ ID NO: 981)
4	Aacgtatcccgacaatccg (SEQ ID NO: 982)	Gagtatttaagggttagtgaaacggttagc (SEQ ID NO: 983)	56-FAM/ caaataacgcgacactaaacgcataattc/3BHQ_1 (SEQ ID NO: 984)
4	Tgttttcggagtcggttc (SEQ ID NO: 985)	Aaatcaaaccgacgatacga (SEQ ID NO: 986)	56-FAM/ ccgataaaacgcgtccaaaccg/3BHQ (SEQ ID NO: 987)

Reagents:

A standard set of reagent and cycling conditions are used for MSP establishment and template amplification. Standard conditions are outlined in tables X & Y. Prior to running biological samples, amplicons were established using 100 picograms of completely methylated DNA as a positive control and 100 nanograms of unmethylated DNA as a negative control. Reaction conditions were also checked for relative sensitivity using 50 picograms of methylated DNA in a background of 50 nanograms of unmethylated DNA. Reagent concentrations are outlined in Table 11 and cycling conditions for the ABI 7700 are defined in Table 12.

Table 11

Reagent	Stock Conc. (uM)	Final Rx Conc. (nM)	MM Conc. (uM)	MM Volume (uL)
Forward	10.0	500.0	3.33	35.0
Reverse	10.0	500.0	3.33	35.0
Probe	100.0	400.0	2.67	2.8
Water	-	-	-	32.2
Taqmix	-	-	-	245.0
Total	-	-	-	350.0

Cycling conditions

Table 12

Temperature	Time (sec)	# of Cycles
(C)		
Denature		1
95	600	
Annealing		50
95	10	
60 or 63	45	

Data analysis

Class prediction by supervised learning

In order to give a reliable estimate of how well the CpG ensemble of a selected marker can differentiate between different tissue classes we can determine its prediction accuracy by classification. For that purpose we calculate a methylation profile-based prediction function using a certain set of tissue samples with a specific class label. This step is called training and it exploits the prior knowledge represented by the data labels. The prediction accuracy of that function is then tested on a set of independent samples. As a method of choice, we use the support vector machine (SVM) algorithm (see e.g. Cristiannini, N. and Shawe-Taylor, J. An introduction to support vector machines. Cambridge, UK: Cambridge University Press, 2000.; Duda, R. O., Hart, P. E., and Stork, D. G. Pattern Classification. New York: John Wiley & Sons, 2001.) to learn the prediction function. For this report, sensitivity and specificity are weighted equally. This is achieved by setting the risk associated with false positive and false negative classifications to be inversely proportional to the respective class sizes. Therefore sensitivity and specificity of the resulting classifier can be expected to be approximately equal. Note that this weighting can be adapted according to the clinical requirements.

Results

To determine sensitivity and specificity of said markers, 50 prostate cancer and 50 BPH samples were screened using the defined parameters. Samples had been pre-screened following a technical criterion of methylated DNA vs. unmethylated DNA. After ensuring they were specific for methylated DNA while not amplifying common unmethylated DNA, assays were run using MethyLight realtime PCR on a TaqMan platform (ABI7900). Final assay performance is outlined in Table 13. AUC and corresponding sensitivity and specificity values were calculated using the SVM algorithms.

Results: Table 13

Gene name	Genomic SEQ ID NO:	AUC	Sensitivity	Specificity
PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE	20	0,921	0,829	0,871
HISTONE H4	36	0,918	0,88	0,719
PR-DOMAIN ZINC FINGER PROTEIN 16	51	0,871	0,768	0,822
ORPHAN NUCLEAR RECEPTOR NR5A2	24	0,859	0,694	0,878
LIM DOMAIN KINASE 1	31	0,868	0,791	0,755
Genomic region	11	0,842	0,815	0,704
LIM/HOMEBOX PROTEIN LHX9	4	0,745	0,695	0,653

We claim:

1. A method for detecting and/or distinguishing between or among prostate cell proliferative disorders in a subject, said method comprising analysing the methylation pattern of a target nucleic acid comprising one or a combination of sequences taken from the group consisting of SEQ ID NO: 1 to SEQ ID NO:59 by contacting at least one of said target nucleic acids in a biological sample obtained from said subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides.
2. The method of claim 1, wherein prostate cancer is distinguished from at least one condition selected from the group consisting of one of normal prostate and/or benign prostate hyperplasia.
3. The method of claim 2 wherein said target sequences are of the genomic sequences as shown in Table 4.
4. The method of claim 1, wherein prostate cancer is distinguished from at least one condition selected from the group consisting of normal prostate, normal tissue from other tissues, cancer of other tissues and/or benign prostate hyperplasia.
5. The method of claim 2 wherein said target sequences are of the genomic sequences as shown in Table 5.
6. The method of claim 1, wherein prostate cancer is distinguished from cancers of other tissues.
7. The method of claim 2 wherein said target sequences are of the genomic sequences as shown in Table 6.
8. A method for detecting and/or distinguishing between or among prostate cell proliferative disorders in a subject, comprising:
 - obtaining, from a subject, a biological sample having subject genomic DNA;
 - contacting the genomic DNA, or a fragment thereof, with one reagent or a plurality of reagents for distinguishing between methylated and non methylated CpG dinucleotide sequences within at least one target sequence of the genomic DNA, or fragment thereof, wherein the target sequence comprises, or hybridizes under stringent

conditions to, at least 16 contiguous nucleotides of a sequence taken from the group consisting of SEQ ID NO: 1 to SEQ ID NO 59, said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and
-determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences, whereby detecting, or detecting and distinguishing between or among prostate cell proliferative disorders is, at least in part, afforded.

9. The method of claim 8, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises converting unmethylated cytosine bases within the target sequence to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties.
10. The method of claim 8, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence(s) comprises methylation state-dependent conversion or non-conversion of at least one CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and contiguous regions thereof corresponding to the target sequence.
11. The method of claim 8, wherein the biological sample is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.
12. The method of claim 8, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises use of at least one nucleic acid molecule or peptide nucleic acid (PNA) molecule comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof.

13. The method of claim 12, wherein the contiguous sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.
14. The method of claim 12, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.
15. The method of claim 12, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules as primer oligonucleotides for the amplification of a sequences selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, sequences complementary thereto, and regions thereof that comprise, or hybridize under stringent conditions to the primers.
16. The method of claim 14, comprising use of at least four such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.
17. A method for detecting, or detecting and distinguishing between or among prostate cell proliferative disorders in a subject, comprising:
 - a. obtaining, from a subject, a biological sample having subject genomic DNA;
 - b. extracting or otherwise isolating the genomic DNA;
 - c. treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;
 - d. contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence of at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, wherein the treated genomic DNA or the fragment thereof is either amplified to produce at least one amplificate, or is not amplified; and
 - e. determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting SEQ ID NO: 1 to SEQ ID NO 59, or an average, or a value reflecting an average methylation state of a plurality

of CpG dinucleotides of a sequence selected from the groups consisting of SEQ ID NO: 1 to SEQ ID NO 59, whereby at least one of detecting, or detecting and distinguishing between prostate cell proliferative disorders is, at least in part, afforded.

18. The method of claim 17, wherein treating the genomic DNA, or the fragment thereof in c), comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.
19. The method of claim 17, wherein contacting or amplifying in d) comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid molecule carrying a detectable labels; and combinations thereof.
20. The method of claim 19, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.
21. The method of claim 17, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.
22. The method of claim 17, wherein prostate cancer is distinguished from at least one condition selected from the group consisting of prostate adenoma, inflammatory prostate tissue, prostate adenomas with grade 2 dysplasia less than 1 cm, prostate adenomas with grade 3 dysplasia equal to or greater than 1 cm in size, normal prostate tissues, non-prostate normal tissue, body fluids, and non-prostate cancer tissue. The method of claim 12, further comprising in step d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group

consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized.

23. The method of claim 22, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having 5'-3' exonuclease activity.
24. The method of claim 22, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case lacking a 3' hydroxyl group.
25. The method of claim 22, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.
26. The method of claim 17, wherein determining in e) comprises hybridization of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof.
27. The method of claim 26, wherein at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.
28. The method of claim 26, wherein a plurality of such hybridizing nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear or substantially so, hexagonal or substantially so, rectangular or substantially so, and combinations thereof.
29. The method of claim 26, further comprising extending at least one such hybridized nucleic acid molecule by at least one nucleotide base.
30. The method of claim 17, wherein determining in e), comprises sequencing of the amplificate.
31. The method of claim 17, wherein contacting or amplifying in d), comprises use of methylation-specific primers.

32. The method of claim 17 comprising in d) using primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides; and further comprising in e) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.
33. The method of claim 17 comprising in d) use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized; and further comprising in e) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at

least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.

34. The method of claim 17, comprising in d) amplification by primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295.
35. The method of claim 17, comprising in d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized, and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295.
36. A method for detecting and/or distinguishing between or among prostate cell proliferative disorders in a subject, comprising:
- a. obtaining, from a subject, a biological sample having subject genomic DNA;
 - b. extracting, or otherwise isolating the genomic DNA;
 - c. contacting the genomic DNA of b), or a fragment thereof, comprising at least 16 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO 59 and sequences that hybridize under stringent conditions thereto, with one or more methylation-sensitive restriction enzymes, wherein the genomic DNA is, with respect to each cleavage recognition motif

thereof, either cleaved thereby to produce cleavage fragments, or not cleaved thereby; and

- d. determining, based on a presence or absence of, or on property of at least one such cleavage fragment, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO 59, or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotides of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO 59, whereby at least one of detecting, or of detecting and differentiating between or among prostate cell proliferative disorders is, at least in part, afforded.

37. The method of claim 36, further comprising, prior to determining in d), amplifying of the digested or undigested genomic DNA.

38. The method of claim 37, wherein amplifying comprises use of at least one method selected from the group consisting of: use of a heat resistant DNA polymerase as an amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of an amplificate nucleic acid carrying a detectable label; and combinations thereof.

39. The method of claim 38, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

40. The method of claim 36, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

41. A treated nucleic acid derived from genomic SEQ ID NO: 1 to SEQ ID NO 59, wherein the treatment is suitable to convert at least one unmethylated cytosine base of

the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

42. A nucleic acid, comprising at least 16 contiguous nucleotides of a treated genomic DNA sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and sequences complementary thereto, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.
43. The nucleic acid of claims 41 and 42 wherein the contiguous base sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.
44. The nucleic acid of claims 41 and 42 wherein the treatment comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.
45. An oligomer, comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a treated genomic DNA sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295.
46. The oligomer of claim 45, comprising at least one CpG, CpA or TpG dinucleotide.
47. A set of oligomers, comprising at least two oligonucleotides according, in each case, to any one of Claims 45 or 46.
48. Use of a set of oligomers according, in each case, to any Claim 47, as probes for determining at least one of a cytosine methylation state, or a single nucleotide polymorphism (SNP) of a sequence selected from the group consisting of SEQ ID NO: 1 to 59 and sequences complementary thereto.
49. A method for manufacturing a nucleic acid array, comprising at least one of attachment of an oligomer according to any one of claims 45 or 46, or attachment of a set of oligomers or nucleic acids according to claim 47, to a solid phase.

50. An oligomer array manufactured according to claim 49.
51. The oligomer array of claim 50, wherein the oligomers are bound to a planar solid phase in the form of a lattice selected from the group consisting of linear or substantially linear lattice, hexagonal or substantially hexagonal lattice, rectangular or substantially rectangular lattice, and lattice combinations thereof
52. Use of the oligomer array of claim 50 for the analysis of prostate cell proliferative disorders.
53. The array of claim 50, wherein the solid phase surface comprises a material selected from the group consisting of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, gold, and combinations thereof.
54. A kit useful for detecting, or for detecting distinguishing between or among prostate cell proliferative disorders of a subject, comprising:
- at least one of a bisulfite reagent, or a methylation-sensitive restriction enzyme; and
 - at least one nucleic acid molecule or peptide nucleic acid molecule comprising, in each case a contiguous sequence at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 60 to SEQ ID NO: 295, and complements thereof
55. The kit of claim 54, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, nucleic acid sequencing, and combinations thereof.
56. Use of a method according to claims 1 to 41, a nucleic acid according to claims 41 through 44, an oligomer according to any one of claims 45 and 46, a set of oligonucleotides according to claim 47, an array according to any one of claim 50 through 53 and a kit according to claims 54 and 55 for the detection of and/or differentiation between or among subclasses of, prostate cell proliferative disorders.

Abstract

The invention provides methods, nucleic acids and kits for detecting and/or distinguishing between or among prostate cell proliferative disorders. The invention discloses genomic sequences the methylation patterns of which have utility for the improved detection of and differentiation between said class of disorders, thereby enabling the improved diagnosis and treatment of patients.

Figure 3

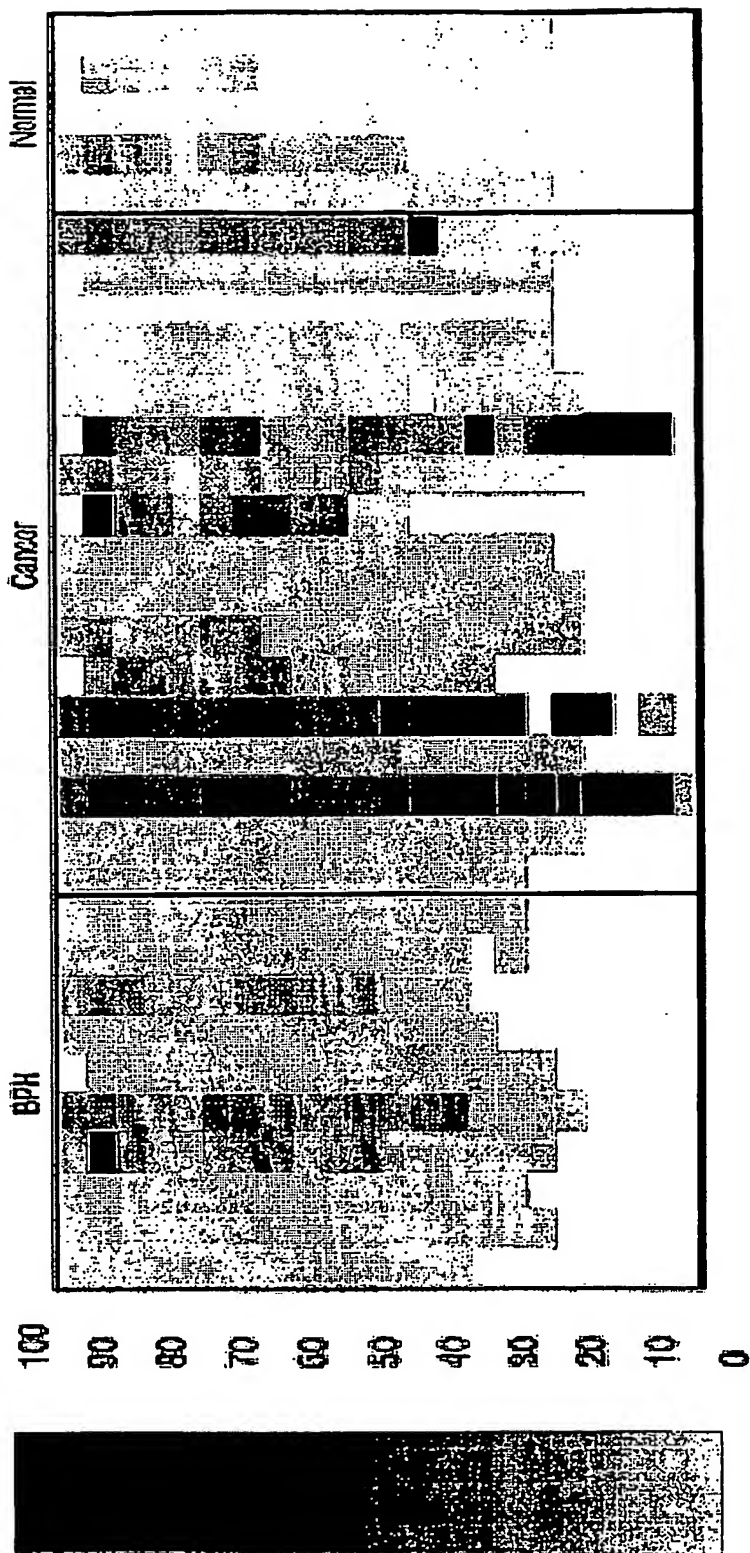


Figure 4

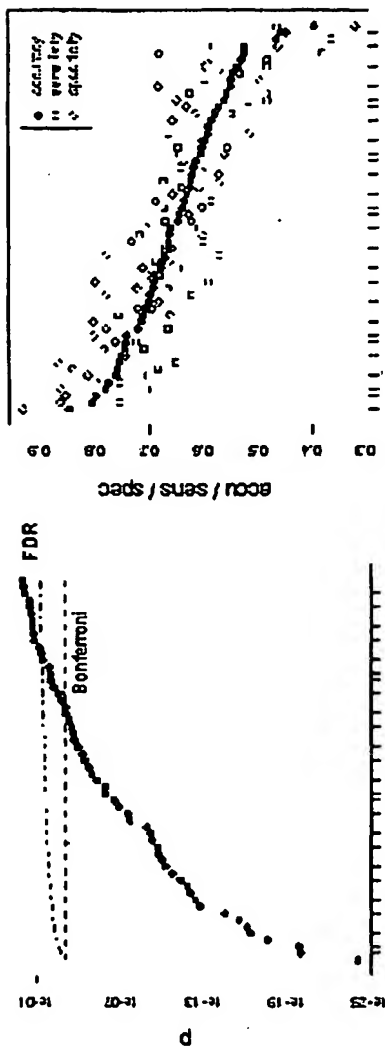


Figure 5

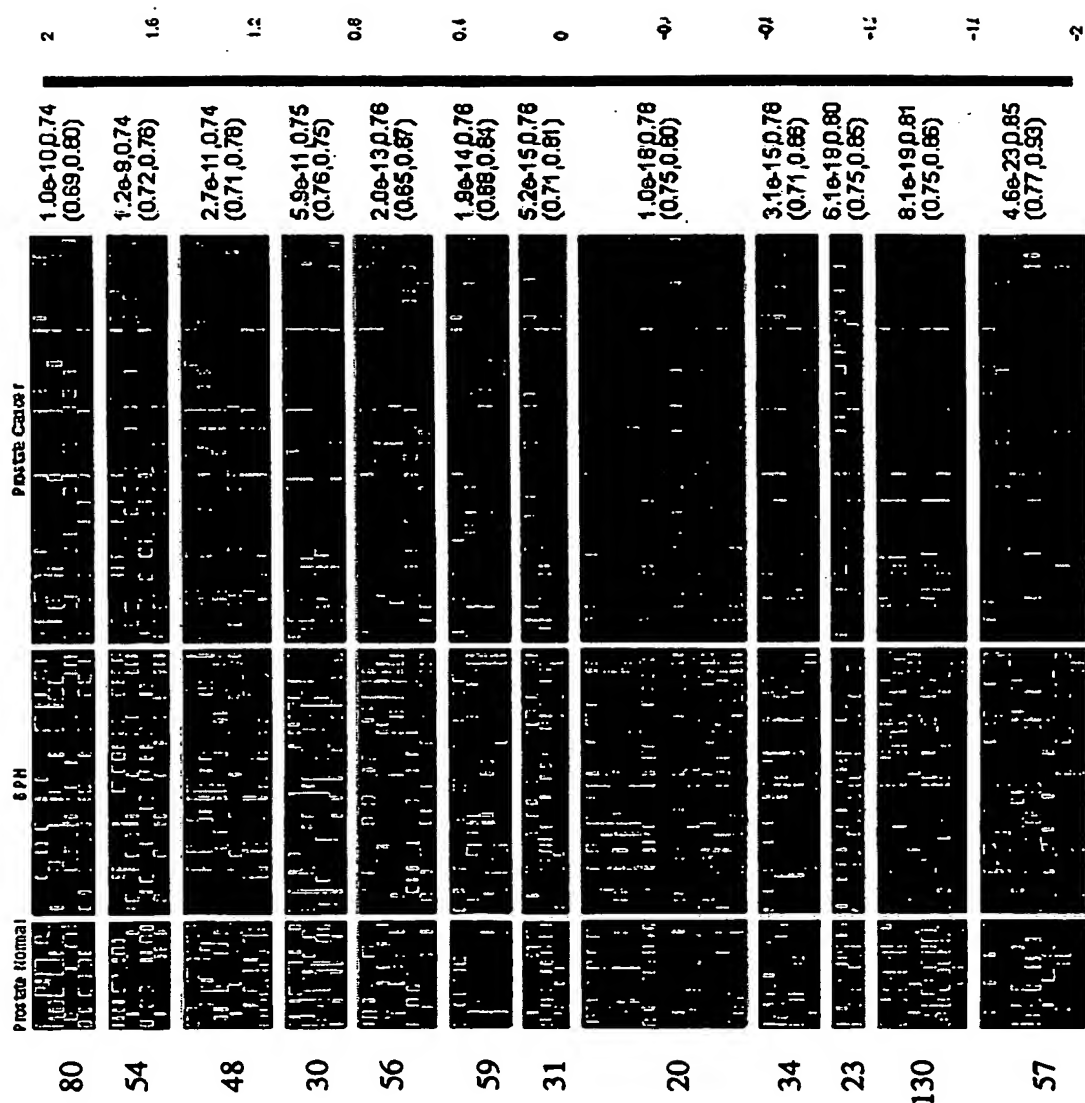


Figure 6

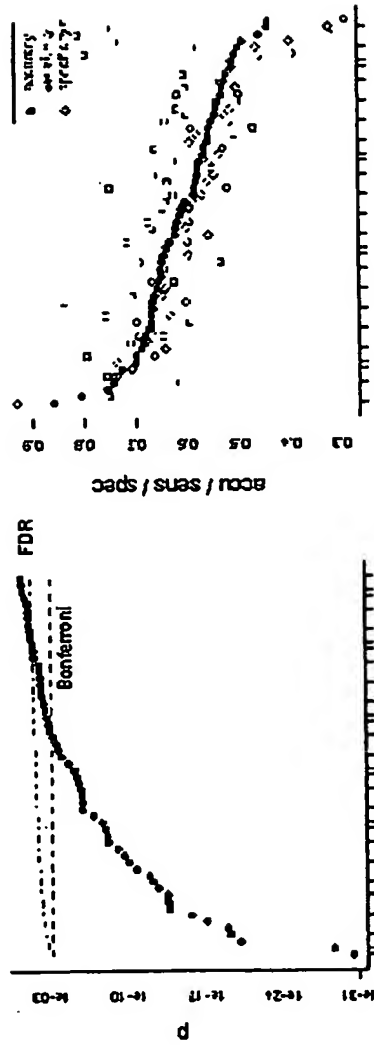


Figure 7

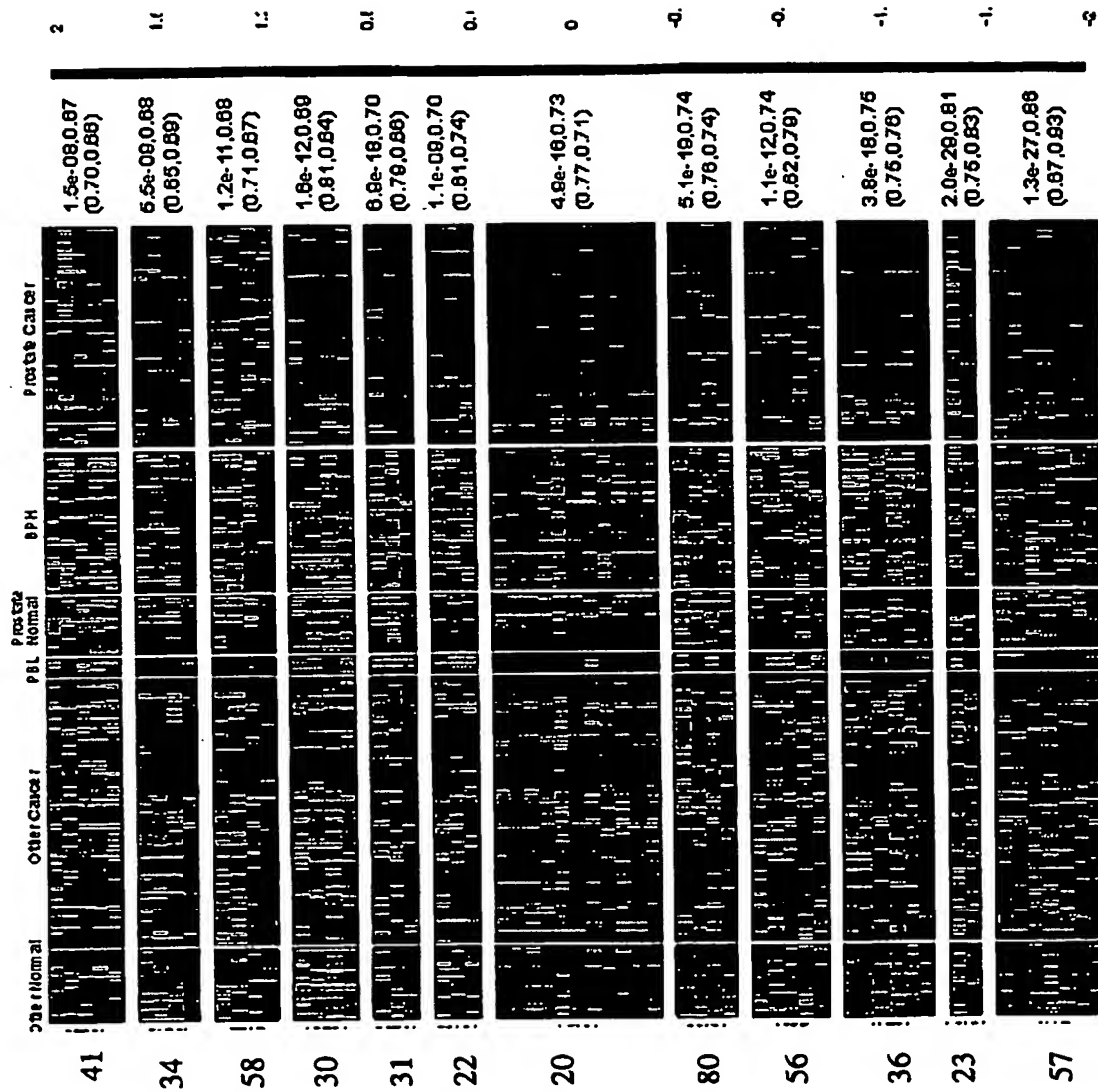
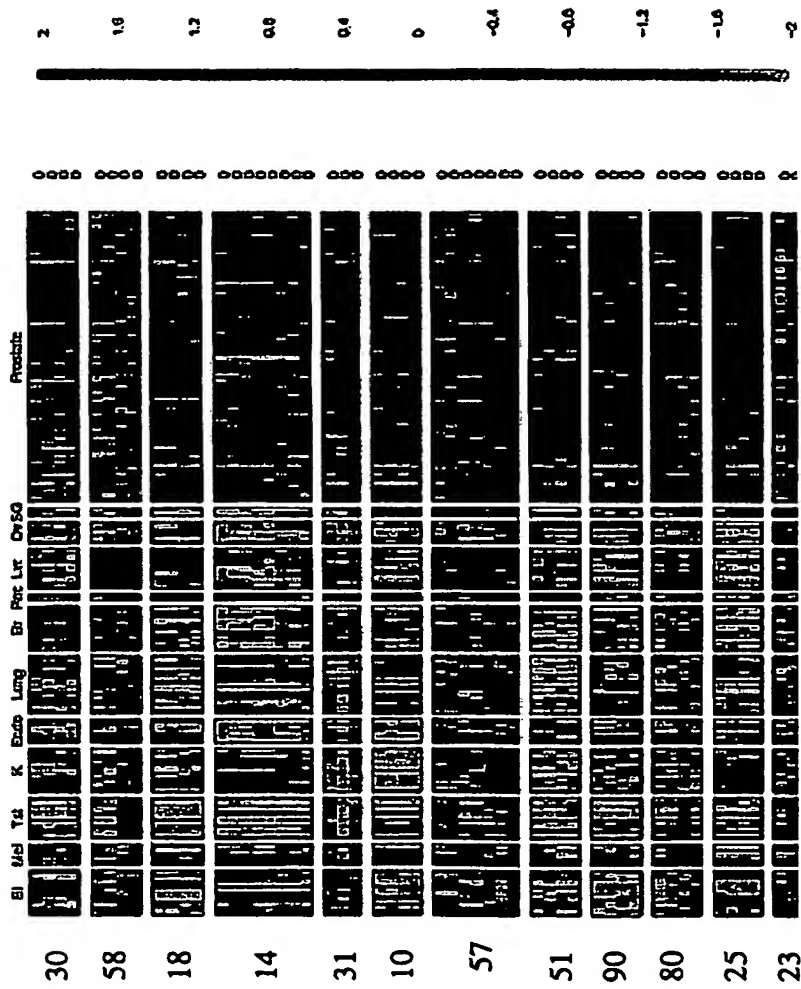


Figure 8



Sequence listing

<110> Epigenomics AG

<120> METHODS AND NUCLEIC ACIDS FOR THE ANALYSIS OF CpG DINUCLEOTIDE
METHYLATION STATUS ASSOCIATED WITH THE DEVELOPMENT OF PROSTATE CANCER

<160> 987

<210> 1

<211> 2299

<212> DNA

<213> Homo Sapiens

<400> 1

```

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ctccctccct gtggcttccc tgccccacc aagacagccc ccaggacctg ggggacagcc   180
agcctgaggt cttctccaa acgaaagaag tccagcctgg ctttaggaa gtgtgtggac   240
atccttgag ttgtctcc ctggagtgg tctgtatt cagatccca tcttccagt   300
gctgggatgg ggaggtctgg ggagccaggc taggtggggg tagctctac ctgggggggc   360
acagcaggca gcgccagccc ggccaggagc tgcaggaaag aagggaacag cctcatgacc   420
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ccggggagcc cctggcacag gaggagaaga gctgagtggg gggctggacg cctccctcac   540
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<13> Homo Sapiens

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<11> 2234

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<400> 30

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<400> 33

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<213> Homo Sapiens

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 <213> Homo Sapiens

<400> 37

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<210> 38
 <211> 2434
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> (1598, 1841, 1846, 1848, 1869, 1871, 1873, 1874, 1878, 1880)
 <223> unknown base

<400> 38

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<210> 39

<211> 2476

<212> DNA

<213> Homo Sapiens

<400> 39

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 <213> Homo Sapiens

<400> 40

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<211> 2555

<212> DNA

<213> Homo Sapiens

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<213> Homo Sapiens

<400> 42

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<211> 2364
<212> DNA
<213> Homo Sapiens

<400> 43

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<211> 2408

<212> DNA

<213> Homo Sapiens

<400> 44

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<210> 45

<211> 2523

<212> DNA

<213> Homo Sapiens

<400> 45

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 <212> DNA
 <213> Homo Sapiens

<400> 46

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<210> 47
<211> 2413
<212> DNA
<213> Homo Sapiens

<400> 47

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2413

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<211> 2171
<212> DNA
<213> Homo Sapiens

<400> 48

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<211> 2490

<212> DNA

<213> Homo Sapiens

<400> 49

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<11> 2418

<12> DNA

<13> Homo Sapiens

<400> 50

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<211> 2351

<212> DNA

<213> Homo Sapiens

<400> 51

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<211> 2427

<212> DNA

<213> Homo Sapiens

<400> 52

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<211> 2501

<212> DNA

<213> Homo Sapiens

<400> 53

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<211> 3190

<212> DNA

<213> Homo Sapiens

<400> 54

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<400> 55

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<400> 56

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<211> 2501

<212> DNA

<213> Homo Sapiens

<400> 57

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<211> 2501

<212> DNA

<213> Homo Sapiens

<400> 58

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<211> 6009

<212> DNA

<213> Homo Sapiens

<400> 59

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<211> 2299

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<213> Artificial Sequence

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<210> 61

<211> 2299

<212> DNA

<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2428

<212> DNA

<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2428

<212> DNA

<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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<210> 64

<211> 2485

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 64

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taatttttt aagtlagagt atatatgaaa tttttttt ttgttatta ttaagtttt 180
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ttgggttaggt gtagtgttt attttgtaa tttagtatt ttgggaggtt gagataggaa 240
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<210> 65

<211> 2485

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 65

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 agaataaaa gtttaagt agtttaggg taaatttat ttggatagt ttttaggt 180
 ttttaatt gttgtatt ttgtcgtg tttagtcg gagggaaagt gttagttt 240
 attagttat ggtttttt cgttggtt aacgtttgt attttttt tttttgtt 300
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<210> 66

<211> 2528

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 66

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<10> 67

<11> 2528

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 67

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<10> 68

<11> 2321

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

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<210> 69

<211> 2321

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 69

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<210> 70

<211> 2412

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 70

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 ttttttcg tttcgtgtt ttcgttagg tagagttcg gtagaaagta ttttagttt 240
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 cggcgggtt ttttagggag ttgggttg agagagtgtt gttttttt ttttttta 420
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<10> 71

<11> 2412

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 71

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 gtttttat gattaggtga gtgttagta aataatttag tttcggtag agagagtag 240
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 gatattgggt tt 2412

<210> 72

<211> 2225

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 72

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 tagtagtgt tattatagt agtggtaatt tttcgtatt tttttcga aattaggata 180
 tttttggcga tttttggaga tttttgggt ttttataatt aaggacggtg ttttaatt 240
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<210> 73

<211> 2225

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 73

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 tcgcgtttg ttgttttg ggtttttt tgattatgt taattgata gaaggtttag 300
 gataaagtt ttttagttg aaaaaaatt tttttttt ttgagatag attttgtt 360
 ttgtcgtta ggttggagt taatggcgtg ttccggtt attgtaatt ttgttttt 420
 gttgaagcg attttttt tttagttt tgaagtgtg ggattatagg ttattttt 480
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 ggggtttt ttatatatt ttattttaa tagatatga gacgtaaagt atgtgggtg 840
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<210> 74

<211> 2205

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 74

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 taaatgagta aaagttaaa aataatgtaa aaagttaaag tcggttgggc gcggtggtt 180
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 ggtgtgtgtg tgagtgttg gtgtgagt ttgttaatt tagttattcg ggaggttag 360
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 gtatttagt ttggcgatat agcgagattt cgttttaaaa aaaaaaaaaa gttaaagtcg 480
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<210> 75

<211> 2205

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 75

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<210> 76

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 76

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 <211> 2355
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 77

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<210> 78

<211> 2380

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 78

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<210> 79

<211> 2380

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 79

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<210> 80

<211> 2308

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 80

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<211> 2308

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 82

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 82

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<210> 83

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 83

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<210> 84

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 84

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<210> 85
<211> 2229
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 85

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<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 86

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<210> 87

<211> 2280

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 87

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<210> 88

<211> 2438

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 88

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<10> 89

<11> 2438

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 89

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<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2403
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 91

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<211> 2311

<212> DNA

<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 92

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<211> 2311

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<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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<212> DNA

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 95

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<212> DNA

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<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2546

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 97

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<223> chemically treated genomic DNA (Homo sapiens)

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<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 101

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<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2222

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 104

<211> 2162

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 104

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<211> 2586
<212> DNA
<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 107

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<210> 108

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 108

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<210> 109

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 109

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<210> 110

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 110

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<10> 111

<11> 2352

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 111

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<210> 113
<211> 2470
<212> DNA
<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 113

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<210> 114

<211> 2305

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 114

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<210> 115

<211> 2305

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 115

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<210> 116

<211> 2234

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 116

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<210> 117

<211> 2234

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 117

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<210> 118

<211> 2317

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 118

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<210> 119

<211> 2317

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 119

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<210> 120

<211> 2553

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 120

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<210> 121

<211> 2553

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 121

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<210> 122

<211> 2381

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 122

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<10> 123

<11> 2381

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 123

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<10> 124

<11> 2514

<12> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 124

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<210> 125

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 125

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<210> 126

<211> 2325

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 126

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<10> 127

<11> 2325

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 127

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<210> 128

<211> 2541

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 128

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<210> 129

<211> 2541

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 129

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<210> 130
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 130

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atttattagt atttttatt aattattgg ttttaggtt ttaagttaa ttattagga  480
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<210> 131
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 131

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gaatgtggaa aatattattt taaaatata gtcgattaaa aaattgttg ggaattgatt 360
ataattattg ataatttta agaaatatag atattaaaa attatttta tttttta 420
agaaattggt taaattataa ttaataaag gaggtataa aattttat ataatattgt 480
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<210> 132

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 132

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<210> 133

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 133

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<210> 134

<211> 2434

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<220>

<221> unsure

<222> (1598, 1841, 1846, 1848, 1869, 1871, 1873, 1874, 1878, 1880)

<223> unknown base

<400> 134

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<10> 135

<11> 2434

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<20>

<21> unsure

<22> (555, 557, 561, 562, 564, 566, 587, 589, 594, 837)

<23> unknown base

<400> 135

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<210> 136

<211> 2476

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 136

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<210> 137
<211> 2476
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 137

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<210> 138
<211> 2520
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 138

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<10> 139

<11> 2520

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 139

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<210> 140

<211> 2555

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 140

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<210> 141

<211> 2555

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 141

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 gtatagaag gtagtgta tagtgatgt ttgtgttcg tattaagga gtgttaggt 2460
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<210> 142

<211> 2516

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 142

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 atttattata taaaattaaa gataaaagt atattattat tttaattgat gtataagagg 180
 ttttcgataa aatttaatat tttttatata aaatttttaa taaattaggt attaaagaaa 240
 tatattttaa tatatatgtg ataaattat agttaacgtt atattaaatg ggtaaatgtt 300
 ggaaatattt ttttgaata ttagtalaag ataagggtgt tttttttat ttttttatt 360
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 aaataggaag agagggaagt aaattattt ttgtttaga tgaatgatt ttgtatttag 480
 aaaaatttat agttttggt taaaagtgt tttaggtgat aaataattt agtaaagtt 540
 tgggataaa gattaatga aaaaattatt ggtattttta tatgttaata atgttaagt 600
 tagaggttaa attaggaatg aaattttatt tatgattgtt ataaaaagaa taaaatgtt 660
 aggaatatag ttaattaggg aggtgaaaga tttttataat gagaattga aaaatattat 720
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agtttaggt ttgatattt atggattgt ttatttgg ttgtgtta ttttttag 2400
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gaaatgaaaa tatatttat gttatggat aggaagattt aatattatta aaatgg 2516

<10> 143

<11> 2516

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 143

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taagatagag ataggagtag tatatacgtg gtttaggttg ggaggacggg tgtaaatatt 240
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ttttattg cgaataattt attttttt tgggttatgg agttttgta ttgttggtat 480
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<210> 144
<211> 2364
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 144

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taagagttaa gtttaggtgc gttatagggt gaaatataaa cgttaaagggt ttataaggta  180
gttttatgg tagggtaaga gtttttatt tttttgtgg tttttgtt tgtttgaga   240
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ggcgtttatt attacgttta gtttagttt atatttttag tagagatggg ggttttatta   420
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aagtgttggg attatagcgc tgagttatta cgtcgggtt agattttga aacgttaata   540
atattgataa ttgggttata aattttttaa aattttgtg tatttataaa taaaaaaat   600
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<210> 145
<211> 2364
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 145

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 gagttaatt ttgtttg ttttggaagt gaattgattg tatatatagt tttgtata 180
 tatatatgt tttttgaaa gtattagtg tgaagagt ttgaaagt ataggagaga 240
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 gaaagtgtta ggaggagagg agttgttgt ttgttggg tggagtcgac ggttgagga 720
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<210> 146

<211> 2408

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 146

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 agaggtcgt atagttagt ttgggggtt gttttatt ataagaggt atatttgt 180
 atagtatt ttattgtt tttttgaa gttcgttag agtggcgaag gtaggaggt 240
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 aaaaatgaa aattaatgt ttttttat atagagatt gttgattt ttatgtatga 360
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 ttgaagaa atattagaat tgggtgtg tggaggtg ggagtata ttggggggg 600
 aagattgt ttttttat atattaggag gtagtgtag gaagggaga ttgtgttcg 660

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<210> 147

<211> 2408

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 147

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 agggagaggt ttatcgtt tttaggtt ttattttt tatgattaa gcgggaggag 180
 agcgtattt tctatagat tattttgaa gcgaggggt gatttaaga gtttttaga 240
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 ttccgttt ttatagggt ttgttttc tagattggg aaaatttat aatttttag 1260

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 cgttttttcg gtaagatta aggttaggga tttttgtt gtaggggat tttatagct 2340
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 ttatgtt 2408

<10> 148

<11> 2523

<12> DNA

<13> Artificial Sequence

<20>

<22> chemically treated genomic DNA (Homo sapiens)

<400> 148

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 tttttttt ttatagatg tttattttg tggtttaggt tggagttag tggcgtgatt 180
 ttggttatt gtaatttta ttttttaggt ttaagtatt tttttgtt agtttttaa 240
 gtagtggga ttataggcgt ttattattt gtttcgttaa tttttgtt ttatagtaga 300
 tatgggttt tatttgtg gttaggttgg ttttaattt ttgatttaa gtgatttgt 360
 tttttagt tttaaagt ttaggattat aggcgtgcgt tattacgtt ggttataat 420
 ttttaattg tttattt attttgggt ttaagatat tattgattgg gtgtagtgg 480
 ttatattcgt aattttaga tttgggaga tggaggtagg tggattgtt gatttagga 540
 gtggagata gtttaggtta gttgtgaga tttttttt aaaaaaatag aaacgttta 600
 ttgatttgg tggatttgg ttatgtttt gttatttgg aggttaggt agggagataa 660
 ttgagttta ggggttaag gtttagtga gttatggtt tttatttga tttagttg 720
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 ggtgtcgtgt ttgttagtt ttgggggtgt gatttttta ttgggggta ttttttat 840
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 tagtcgggag cggtaggtt ttttttga ggttcggag ggagtgtgtt ttgcggata 2460
 ttgcattt aggttcggg tttaggtt ggagggtcg cgtttcgtg gtttagttt 2520
 tta 2523

<210> 149

<211> 2523

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 149

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 aggtgtcgt aggggtatat tttttcga gttttagg gagggttta tggttcgt 120
 ttgttagtta ttctgtgtgt tttgggtt ttttttta gttttgtt ttgacgttac 180
 gcgttcgatt tttttgtt gtagtagtt ttttataag gtgtcggtc ttgttttgg 240
 gattttttc gttcgattt attttaalc gattattat aaagatttta ttttagtgt 300
 tctaggtat tgggggttag ggttcgata tacgttttg gaggggttta attaattta 360
 ttttattgt tttagtgt tgggggttgg gatttaatt ttccgttgg tctagtgat 420
 tattgggata tatgtttat tagttagtt ttttcgggg tttaggttt agttttatt 480
 attttttat gaggattatt tgggggttta gagaaggagg aggtagtga ttgtcgggga 540
 gatggagttt cgggggagg gcgggttta ttttattg ttggttgtt gggtttatg 600
 gaggggtat ttgagattt ttttaagag ttggtttt ttttttagt agagttaggt 660
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 aaaaaagatt atatatgagt ttaaaatgat taaagagala aaagtagaaa tgaaaaaataa 2460
 tataatagta tgaaaaggat ttatagatt agaaaaataa ttatatagga ttttaatac 2520
 gag 2523

<210> 150
 <211> 2280
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 150

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 aggtcgttgt ttacgttttg agtgcggac gaggttaata taggttttct gttatagaat 120
 atgtttgggt aggaagatcg gaatatitgg ggttgggtat ttatcgtttt ttacgggtat 180
 atacgagtcg ttagggaat gtctgtttt gtgtgtgttg tacgtgtagt ttittgggta 240
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 attgtttttt ttittcgtg acgtagggtg gcgtgggttt ttttttagt ttittgtcgg 360
 tgtgttacg tgagaagggt tcgggtgtcg gttcgttat ttccgaattg tgggtttatt 420
 tgaagttaga ggttaaattt ttacgggta gtgggacgtt agtcgtttt gattttttgg 480
 ttaagtgggt ttgtcgtga ttctgagaa tgttaagtg ttaatgtgtt tcggggggta 540
 gggcgggggt tgggatttta gtgtgtgtt agttttttt tcttttttc ggggtttatt 600
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 ttaagggga tctttttt gttgttagg aaggtaggt agtaagaagg gtctgtcga 720
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 cgttaattt aggagtgag aaggaaatg gaggatttt tggaggtgt aggttaattg 2160
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 aaagaaggta gaaggagtc atgggtttt taggtcggaa attttataag tattaggatt 2280

<210> 151
 <211> 2280
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 151

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tattaaatt gttatttta gagggtttt tagttttt tttatttt gaattgagcg 180
aagcgggtgc gattttatt ttgggttac gagttttgc gtattggga gattttgaa 240
tatttcgga gaagttgaa agtttcgga gatggttcg ttgttttg tattagatcg 300
ggtttgtaa aggatgtatt ttccagatt tttttgta cgttagtg gggttttc 360
gattttatt gagggattta ttggaggaga ggtacgggga tgtgtttga gtacgggatt 420
ttttggcgc ggagtaggt gtttttagt agagttcgac gggttttt ttgggtgt 480
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agagagttt ttttttaa gtttttat cgaatttat ggtcgggtcg ttttgatcg 600
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aaatagtat tacggggaac ggttcgttt taagataatt tcggggatat ggataata 720
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tcgggtcggg tcgggttgg ttgtcgtt atttcgtta gaatcgttg ggtacgggtt 840
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ttaagaggt aaaggcgt ggcgtttt tgaatcgt ggggttggt ttaattta 1860
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gttcgtgg ggagcgtg atgttagt ttaagtgtt cgattttt gtttaatat 2160
attttgac gaaagtta tgttatc gttcgttatt taaggcgtg gtagcgtt 2220
aacgttgtt gcgggaatat agtcggtt aatgtatt ttaagataga taaaatgt 2280

<210> 152

<211> 2413

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 152

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acgtggttc ggcgtgtt aaaattagt ttttaggt cgtttaatt tgatttgt 120
tttaagggt taaagtag ttgtttt tagagggtg ggaagtagt tgtttttt 180
atttaggat atacgtat ttatttta taatatag gtatatat atttagttt 240
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gattttaacg ttatatat atatttgt ttataaat tagggtata tatatttc 360
gtttatga tgttaggt tcggcgtt ttattttt gttattgt ttgttgtt 420
gtttatg gtgagatag atgttgtt tagatttat cgttttcgt ttatttgt 480
tgggtatga tgtgttag talagtgt ggtagttt gggttttt taggtaggt 540
gttcgatt tcgtttat tgtatga tttttgag gttattat tgtgattt 600
acgtagggt alatttgt tattgtag ttttaagt tatttgtt attgggtt 660

gttttatntt gtttaattta ttttggctg gattttttg ttacgtttt tagtatcgta 720
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 aatatagtt tagcgggaacg agattaggtt ttgttttta ttccgggttc gtcgagggga 1020
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 aggcgtgtga ttucgttt tttagttt ttttttatt tttagtggg ttattttta 1200
 gtttaaatag ataaattgt ttaaaggaat aaggattagt aggttacgt gtgcgtatgg 1260
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 aattgataag ttt 2413

<210> 153

<211> 2413

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 153

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 atgggttagt tggggagtg ttattatgt agtgaggta cgttttcga ttcgttacg 120
 tgggaggatt ttttttatt tagattgat attttttag ggtttttt ttatttagg 180
 tcatatttt tttaagggtt ttcgtttatt tagaggcgt attttttag ggttttcgt 240
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 ggttttcgt ttattcggag tcatatttt tttaggggtt ttttttatg tagaggtgat 360
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 tticggtagg tgtgttcgt ttgttttt ggtgtggtt tttttatta gtatttttg 600
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 attcaggggg ttcgttttt gatttaattg taccgttata ataatttat ttcggtggtt 720
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<210> 154

<211> 2171

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 154

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<10> 155
 <11> 2171
 <12> DNA
 <13> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 155

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<10> 156
 <11> 2490
 <12> DNA
 <13> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 156

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<210> 157

<211> 2490

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 157

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<210> 158

<211> 2418

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 158

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<10> 159
 <11> 2418
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 <13> Artificial Sequence

<20>
 <23> chemically treated genomic DNA (Homo sapiens)

<400> 159

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<210> 160

<211> 2351

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 160

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<210> 161
 <211> 2351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 161

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<210> 162
 <211> 2427
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 162

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<10> 163

<11> 2427

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 163

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<10> 164

<11> 2501

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 164

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<10> 165

<11> 2501

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 165

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<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

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<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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Figure 1

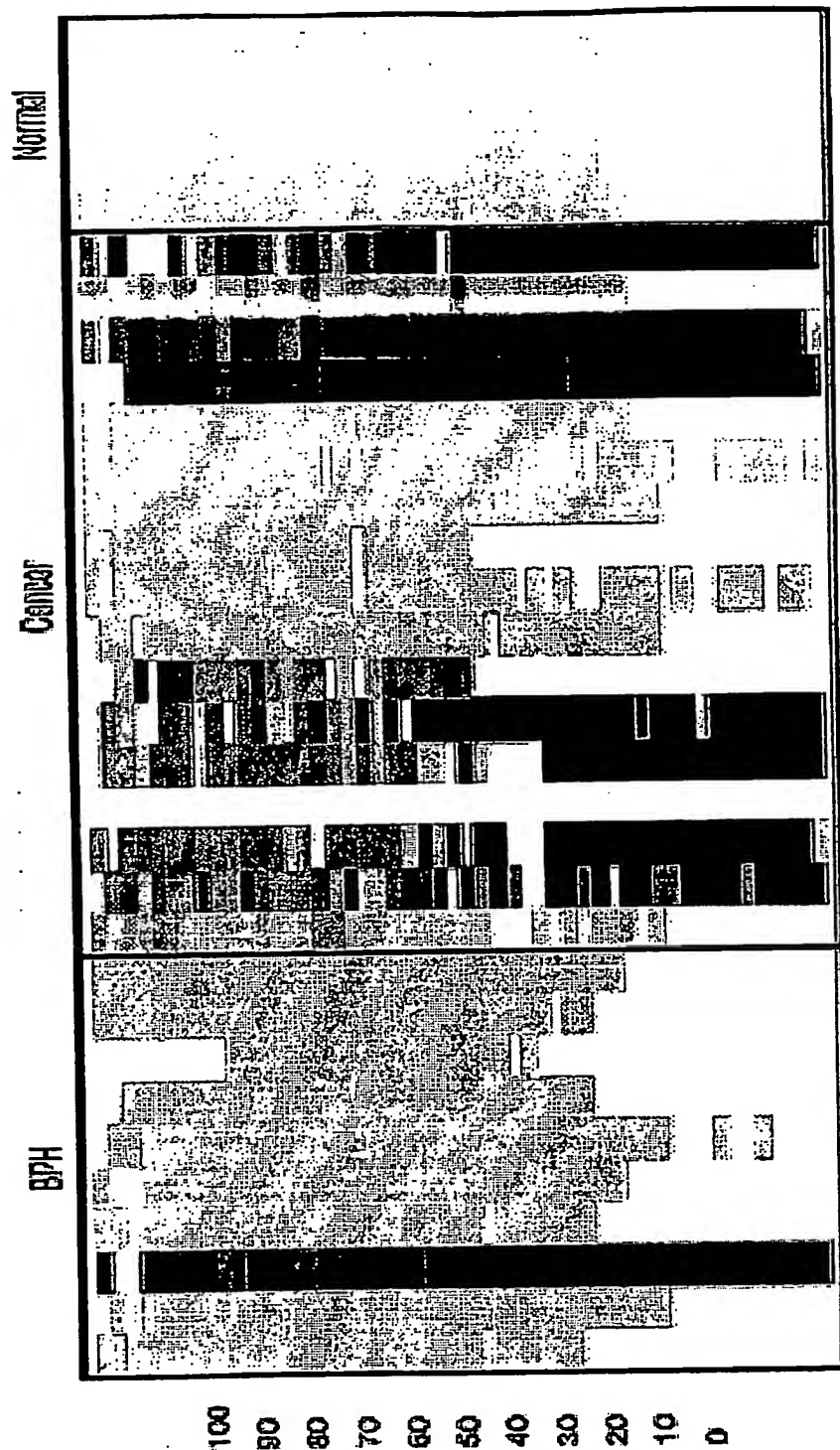
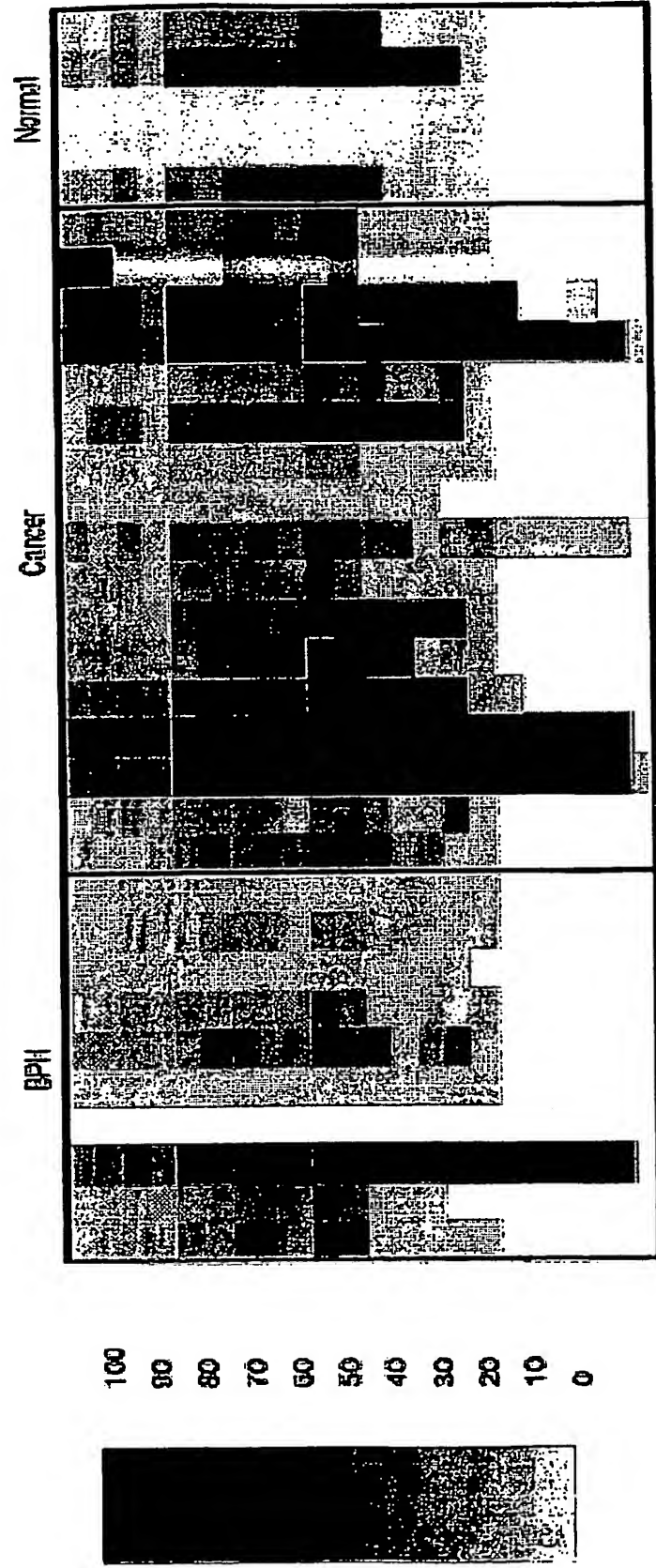


Figure 2



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<220>
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<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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 <223> chemically treated genomic DNA (Homo sapiens)

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2501

<210> 171

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 171

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aatgcgcgt cggtagttg ttaataaat tttttttt tttttttt tttaatta 240
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<210> 172

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 172

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<210> 173

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 173

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<210> 174

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 174

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<210> 175

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 175

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gtattggg ttgaggtt ggtttttt gtttttgt ttgtttgt aatgtagtt 240
gtagggtta ttttaggt ttgttttt tttatagt atttattt ttagggtta 300
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<210> 180
 <211> 2428
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 180

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<210> 181

<211> 2428

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 181

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 ttgtgttgt ttatgaaat agagatttga tttagtaat tattgttta taagatggga 420
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 ttaaggata gttttttta atgttgt 2428

<10> 182

<11> 2485

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 182

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 taatatttt aagtagagt atatatgaaa tttttttt ttgttatta ttaagtttt 180
 ttggttaggt gtagttgtt atttttgtaa ttttagtatt ttgggaggt gagataggaa 240
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 aalaggatg tataaaaaag gtgttagtg ttaagtagg ttttagggg aagtgattt 840
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<210> 183
 <211> 2485
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 183

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 tttaattt gttgtatt ttitgtgtg tttagttg gagggaaaagt gtgtagtttt 240
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<210> 184
 <211> 2528
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 184

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tttgatgtt ttgttttt tgggttagtg tttatattat gtgagtgtgt gtgtgtgtgt 180
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tttgtgtt 2528
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<210> 185

<211> 2528

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 185

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<210> 186

<211> 2321

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 186

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<210> 187

<211> 2321

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 187

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<210> 188

<211> 2412

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 188

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<210> 189
 <211> 2412
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 189

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 <211> 2225
 <212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 190

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<210> 191

<211> 2225

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 192

<211> 2205

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 192

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<210> 193

<211> 2205

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 193

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 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 194

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<210> 195
 <211> 2355
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 195

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<210> 196

<211> 2380

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 196

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<10> 197

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<23> chemically treated genomic DNA (Homo sapiens)

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<210> 198

<211> 2308

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 198

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<210> 199

<211> 2308

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 199

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<210> 200

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 201

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 201

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<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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- <210> 203
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- <212> DNA
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- <220>
- <223> chemically treated genomic DNA (Homo sapiens)

<400> 203

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<211> 2280

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 204

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<211> 2280
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 205

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<211> 2438
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 206

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<210> 207

<211> 2438

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 207

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<210> 208

<211> 2403

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 208

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<210> 209

<211> 2403

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 209

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<210> 210
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 210

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<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 211

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gaaaatttg tgtttttt ggtttatag a 2311
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<210> 212

<211> 2271

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 212

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<10> 213

<11> 2271

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 213

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<10> 214

<11> 2546

<12> DNA

<13> Artificial Sequence

<20>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 214

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<210> 215

<211> 2546

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 216

<211> 2251

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 217

<211> 2251

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 217

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<210> 218

<211> 2413

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 218

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<210> 219

<211> 2413

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 219

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<210> 220

<211> 2222

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 220

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<210> 221
 <211> 2222
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 221

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 <211> 2162
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 222

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<210> 223

<211> 2162

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 223

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atattagtt agagtatt gtgttttt aattatgt tttgtgtt aggtgggtt 240
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attaaatt taagtttt ttggaatga gagaggtata aaagtgtt tttagtagt 540
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<210> 224

<211> 2586

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 224

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 agggataag ttattttt ttattttt gtttttag ttgttagga gttgggggtg 540
 ggagtagt gtttttta ttgttttt ttaaaattg agattgaaa atagggagt 600
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<210> 225

<211> 2586

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 225

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 ttttttgg ttatagatt ttaggatgt ttataggga gtgagttag tagagtgg 240
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 ttggtg 2586

<210> 226
 <211> 2257
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 226

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 attgttagt tggatatt agtgaggat gtttatga tagggatgaa gattttgag 660
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<210> 227

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 227

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<210> 228

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 228

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 agtttagt aattaaatt tttttt aaattttt gtttaggt tttttgtt 2160
 tttttt ttgtttt tggaggttgg gttggtagt gttttttt gtttttag 2220
 agggagtga gttgggtg tttagttta tttttttt gttttgggt tgaagtatt 2280
 tttttt agttttga gttgttggg tttagttt gtttttatt gttttttaa 2340
 tttttt tt 2352

<210> 229

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 229

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 attgtattt ttttgggtt atagagagag atgttgttt tttttttt ttttaata 180
 aataataaa taaataaaa aaattttg agttgggtat ttatagagaa aagagttga 240
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 taggaagtt taattgttg tggaaagtga agtgggagta gttttttt atggtttag 360
 tgggaatgag aaagatagag taggttggg atatagttaa atgtttatt ataatttga 420
 ggatagttt agggaggatg ggtttaagt atttatgaga aatttttt ttatttag 480
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 ttggagggt tgtgttgt ttattttt tttaagggt gtgtagggt ataggttta 1920
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 gtagtagggg tg 2352

<210> 230

<211> 2470

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 230

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 tttaaaatt tggggaaaa tttaaatg gagaaaaaa tttaattta gttattta 180
 tataaagtat taaaaatatt tttagtagt ttgtttaag tttttaggt tagtggtagt 240
 atgttagtta aaatgtaatt taaaatgaat gaataatagt tagttgtag atattgatg 300
 taatataata tggaaatata ttggaagtat tttaaaatt aatatttga ttgtgaatg 360
 tttaaatlaa gttatttaa ttagggtttt attttgaaa taattattta aaatatgtt 420
 tgggtgtaag attgttagt attttagga aatttttta atggtttaa attttaggt 480
 tttagaagggt gtgattgatt aggttaaat tatattttt ggttttag ttgttagtt 540
 aggtagttaa tttaaaat tgggggtgga tgagtattt gaagtttaga ttaaggagt 600
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 gttgtagtga gttgagattg tttaattga tttagttg ggtgatagag tgagatttg 2400
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 gatagtgtg 2470

<210> 231

<211> 2470

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 231

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 ttgtttgaga taggggtttg ttgtttgt taggttggag ttgtgtgaa ttatttgg 120
 ttattgtaatt tttgtttt tgggtttaag ttattttt attttatt ttgaggagt 180
 tgggattga ggtgtgtgt attatgttg gttatttta tttttgtg aaatgagatt 240
 ttatattgt gtttaagtt gtttgaatt gttgagttta agtgattgt tagtttgg 300
 ttttaagt gttgggatta ttgtgtgag ttattgtga ttggtttaa atttaattt 360
 gtagtggg gtttaagat gggaaagtt ttaggttgg gtagttagg gggaaagtt 420
 tttttgtg atttaaaaa atgttttta gaaaggagga aaggtgggt tttaattgt 480
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 ttattgtaaa tatgtggata tttttttaa tattagatta ttataagat aaggagtata 600
 ttgtgtgaa aattttttt gtttagttt tttaaggtt ttatttgt ttttgtat 660
 gtagtttga aaattgtta agggaggtag aggttaagt ttatgttg ttatgtga 720
 ttattgtag ttgtgggtgaa ggttgggtt ggaaggatgt ttttagaag gtttttag 780
 ttatgtgtt tttttttg ttatagggt ttgtgtgtg attttatta ttatgttt 840
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 tatttaggt tagagtgtg gtagtaagtag aatgtgtga gtttgggtt ttgtgtgt 960
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 ggtagtggag ttattggat ttgggaatt atttgggtt ttgtgttga ttatgttt 1260
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 aatttggga aaagtattat aataaatgta ttatttttt gtttaaaag aaaaattaat 2400
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 ggttggttt 2470

<210> 232
 <211> 2305
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 232

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 gaataaaatg tgaatttag ttaataatag tgaataat tggtttatta attgtaataa 180
 atgtattata ttagtatgag atgttaataa taggggaaat tggatgttgg gtatatggta 240
 ttattttat taaataaat tatattaaga aaataatatt ttttttaaa ggtgtagtga 300
 ataaaaaat ggttatttat atatttaata ttgggttaa taatggtaa tatagttaaa 360
 gttttttt attgttttt ttattaga tatgattgt tttttaatt tgattttat 420
 tttttgat ttttgattt ttttaattat atagtatgt ataattaagt aatatatgt 480
 attgtttat aagttttaga gttgaatgta tatgaattgt tatattattt attttttat 540
 attttttt ttgtttta ttattttt gatttagtt tttttatt ggtgtataat 600
 attatattt aatatttat aaggatttta ttgtttatt gatggatgtt ttaattttt 660
 tgttttatt tatagtgtt ttatgtatat ttgtttat ttataaagt tttataaga 720
 tatataggta ggagttaggt gttgggggtt agtaattgaa aattttatt agattttgt 780
 atattgttt ttaaaaggagg ttttaattt tgttattta tttagtggtg tgtatgtta 840
 gatgtgtgga ggagaaatta tttaaagata tataaattag ataataatt tgtttttt 900
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 ggatttagt gaggattat ggtt 2305

<210> 233

<211> 2305
<212> DNA
<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 233

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ttaaattat ggtaattagg atttattata aagagtaatt ttagtttgt ttgatttgt 180
tgatgttat aaatiagata aaatgatga ttaggttaa atgttttt ttattaaag 240
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tttaaata tttttttt gttgattat tatgtgggt taaaattta aaaatagttg 360
gaaattgtt tatgtattaa ttaagggtg tgagggtta ttatttaga tgatttggg 420
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tttatagat ttatgtaga ggggtatt atagtattg agatgagt atgggaatat 660
aaaaagaat ttttaaga ttaattgag ttgtttatt itaagtatt tagtttgt 720
ttttgtaa atgttttt taggggtgt aatattgag ttgggttt agttatgt 780
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<210> 234
<211> 2234
<212> DNA
<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 234

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ggggagggtg gttttagggt gttttttt tagttttt gtggggttg tattagatt 240
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 agattgagag atggggaaat gtgaaggag agaagattt ttgtttt ttaggtgt 2040
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<210> 235

<211> 2234

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 235

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<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 236

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<210> 237

<211> 2317

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 237

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<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 238

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 239

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<211> 2381

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<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<210> 241

<211> 2381

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 241

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 aaatgtatg taggttgtg ggttttgt ttgttgtt tgaattatg tattgttg 960
 tattgggtt ttgttttt ggttggtg ggaaggttga gtgtgagaaa ggagtgagg 1020
 aggtttagg tagagtga gttgttat ttggagaag gtgtgttg ttgtgttg 1080

atggtttagg ttgtgggttt ttgtgtgggg atgtgtgtgt gtgtagagtt gggtttgggt 1140
 gggtaggtg ttgtgggtg ggtgatgggg atttagggtt ttgtttgtg attttttg 1200
 ggttgtttt ttgggtttg attgtttgt taggtttgt gtagggttt ttgttttt 1260
 ggttggtagg tgtttgggtt gtaggtgggt tggtaggtag gtgttagtgg gaaggagta 1320
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 ggggtttgag ggggtggagg aaaggatagg atgttggatg gtgtgtttt ggtgggagat 1440
 gtgtgtgtg ttatgagt gagttgtt ttgtttta gtggttagaa gtggagggt 1500
 gaaattgggt ggggtttta ggttaggatg ttttggga gtgtagtgtt gatttaaggt 1560
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 tgggtttgg ttgtttgt gatagtgtt ggttgggtg gaagaatgga tgttttgag 1860
 aagtgtgtgt gtttggagg ttgtttta ggggattgga gtttggagag tggtaagggt 1920
 ttaaggtag aggttgggtt aagggtttt aggggtttt tgggtgtgt ttttgggtg 1980
 gtgggttaaa aggttgggtt gtaggagtg gaattgaat ttatgtttt aggggagatt 2040
 gtgattgaa tgtagtgtt tagattgtt ggttatttg atgtgtgtt ggggtgtgt 2100
 gtgttgga tgggtggat ttgtgtga ttgtgtgt tttgttgtt gttgtttg 2160
 gttgtgtg taattatgg atgtgtggg tggagtgggt gtaagtga tggagtgtt 2220
 tgggttgtt gtggatgtt ttgtttt atttggtt taaagggtt gtgtgggtt 2280
 ggttgtgtt ggtgtatgt ttgtttt ttgtttgt ttgtgaatt ttaggggtt 2340
 gtgttttg ttgttagga gtgtgtgtt gattgtttg 2381

<210> 242

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 242

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 tatattata ttattgttg ggtttttg gttttaata ggattaaatg aatgttttg 120
 ttttatgat tgtatgttat gtagagagt taagttagtt aatattgtt attgggatg 180
 aaggaaatga ttagggaatg taaggagat tagaagttag aattttgaa ttgtaaat 240
 tttttttt tttttttt ttlttgat agagtttgt ttgttgtt taggttggag 300
 tgtttatgt aattttgt ttlttgat aagtattt ttgttttg ttlttgaga 360
 agttgggtt ataggatgt taattttt taatttaat agagatagg ttatttat 420
 ttgttaggt tggtttaaa ttlttgat taggtatt attagtgtt gttttata 480
 gtgttggat tatagggtg agttatgt ttgttgtt aaattttta ttlttgat 540
 atattaat ttgtttata aatagtatt taattttt agtaaatgt gtgtttata 600
 ttgattgtt tgggtttt attgtttt ttattgtt gtgaatgag ttattata 660
 attagtagt gaaaataga gatattat atttatata gttgtggag gtaggaatt 720
 taggaggtt ttgtgggtg atttgggt ttatgtggg ttatagggt taatgtgt 780
 ggttgggtt gtagttat gaagtttt ggggggaagg aggggttt ttgtttg 840
 gaagggtg gtgtttat tatgtttt ttlttatg gttataggt ttatagaagt 900
 aaagggtg tatgttaga ttgattgag tggttttt ttlttgat atagtatt 960
 atagatag taggggtgt attagggtt ggtgggtt gtgattag tagggagta 1020
 ttlttgtaa attgtttg gtagaggtt gttgtttt atgtgtgg agatgatga 1080
 gtgtgttt ttatttat ttattgtt ttgtatt ttgtgaga ttattgtt 1140
 ggtttttg ggggtttt tttagaata ttattttt gttttgtt gttgtgag 1200
 gttttatg ggtttttt tgataatt ttatttgt ttgttgtt gttgggtt 1260
 ttgttgtt taggaggtt tttaggtga ttgttgtt ttgggttt ttatttat 1320
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 ggaggagat gttatttt tggaggataa gagggtgtt atttatagt ttlttatg 1440
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 agagaggtt gttgtgtt gttttttg gtaggtggg tgggtttt ttgtagt 1560
 tatattat ttlttatgt aggttttt ttatttat ggagggttt taggattt 1620
 gttattat gtttagat aggttagat ttatttat atttataatt ttgtttt 1680
 atatttgtt gttgtgaga ggaagatgt ggtatttt gttttgtt tttaggggt 1740

tgggtgggg tggggttgg tgaattgat ttgggtggg ttgtgattt tgggttta 1800
 tagtgagtag ttgtgta aaagtgtt attggattag ttgggtttt gatgtagag 1860
 ttgtagtgg tgttaggag gatgaattg tgtgatgtt ttgttagt ggttttgg 1920
 ggttttga gtgttttt gtgattaga ggaagtgtt ggttagtag gtgttttt 1980
 ggggtgtt agtatttt ttgttag tagatgttt ggggtgta ggttttgg 2040
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 ttggtagt ttgggggt ttattgtg tttttttt tttaggtt tggattgtt 2340
 ttgtatgt aataaattt gtttagtt tttagggga attttggga ggtagggaag 2400
 taggggag taggaattt ttgtattt ttgggggt ttgggtagt ttatttt 2460
 ttgtaaag ggggttgg ttgaataat ttgaaggag ttgagtggt ttat 2514

<210> 243

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 243

atgaattgt ttgttttt taggaattt ttgaataaa atttttgt agaaggatgg 60
 gagagtgt taaggattt agggagggtt agaagagt ttgttttt ttgttttt 120
 ttttttag gatttttt gtaagggtt aggtagggtt tttgatat tagagaatgg 180
 tttaggttg gaaggaggg ggagtata gtaagggtt tttaggtt tttaggttt 240
 ggggttgg ttattttt agtagaagta atagggttaa gttattgta gtagggttat 300
 atagatttt gagaagggt aggttgggtt gttgttagt attttagt ttgttttg 360
 tttgttga agttgttag aaggattgt ggggagtag ttgttagtg gtaagggtt 420
 gaggagtga gtttaggtt agggattag attgtttg agttgttag gttgttagg 480
 ggttgtgt atttagat ttgtttgt aggaagtgg ttgtgggtt tttaggttg 540
 ttattgtt gtttaggt ttgttttt ttatagat taatttagg gatttagga 600
 gtgtttga gtaggata tatatagg ttgttttt ttgttagtg tgggtttgt 660
 ttgtgggtt ttgttaatt taataagtag ttgtgtta ggaattgtt attgtaata 720
 ggttaggtt taggttagt taggatgag gtaagtgt ttatttag tatagattt 780
 taggattag gatttagg ttgttaatt ttgttttt tagtattgt gtgttagg 840
 gttaggtgt ggtgagtg gtgaggtt ttgtgtt agttgtggg tagtaaggt 900
 ttgaaagg tttaagtga taggtaat ttgtatgt ggggtatgt ttgtgttt 960
 atagagaata gttattgt ttgttgga ggttaggtt ttgtatatt ttgttaatt 1020
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 aagagtgt ggtgtgtt ttgttttt tttagaagt aggtatgtt tttagttt 1140
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 tttaagggt tagggattg agttattgt ttggaaatt ttgggtgtt gggaggttt 1260
 tgataaat agtgatggg gtgggtgtt attaaggag ttgttttag aggttttg 1320
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 ttgttttt tttaggtt ttgggttata gttggataa gtgaagtta ttgtgtgt 1440
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 tttagttg tttagttt gttttagt ttgtgtgt ttgtgtgt ttgtggaaa 1560
 ttgttggt agaggttgg attgttag ttgtttga tatgttag ttattttt 1620
 gtaattgt gaattgtg gaggagag ttgtatggg tagtttagt tttttagt 1680
 ttgggggt ttgtttt tttaagg tttaggtga ttgttttt gtttaata 1740
 ttgtttat gtattttt gtataatt gaattgtt tttagttt ttgtattt 1800
 ttgttttg ttgtgtgt agataatga ttgtgtgt ttgtgtt aagttgtg 1860
 gtaattgt tttagtaatt gtaataata ttgttaggt attaggtga ttatagag 1920
 gttatttt tttaggaatt attgatgt ttatttag gtttaggt ttgttagt 1980
 aaaaagaag attgttagt ttgttaggt gttttatt tttaattt gtattgtg 2040
 aggttaggt ttgttaggt tttaggtt ggttttag attagttg ttataggt 2100
 gaaattgt ttatttaa aataaaaa attagtag ttgtattt agttttag 2160
 gagggttag taggagaatt gttgaatt gggaggtga ggttagtg agttttag 2220
 ttgggtat aaggtaga ttgtttta aaaaaaaaa aaaaaaaaa aaagattt 2280

tagatttaag aatttgatt ttaatttt agtatgttt ttatgtgtt tttttatt 2340
 taatgagtg ttttaattaa ttatgttt tagtgtaata tttatattt ggaattaaga 2400
 tatttaatta atttttttag tagttaaga aatttaatag tgagtgtgag tgtgtgtgtg 2460
 tgtgtgtgtg tgttgtgtg tgtgtgagag agagagagag agagaaagt gggg 2514

<210> 244

<211> 2325

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 244

agtttagta gtttggttg gttgtgttg tggtagtagt agtagtggtg gtgtgtgtg 60
 tgggtgtttt ggggtatttg tagtattatg tattgtttg tattgtatt atttataatg 120
 tgggtgattt gtggagattt tattgttta ttatgggtag ggtgggggtt tgggtattt 180
 gtgtttgtg tttttgtgt ttgggagta aatttttat ttttagtga ggaagtgga 240
 gttggggat aggggtgaaga gagaggatgg gtttttagtg taattgtaga gttagtata 300
 gaagtttat gaaagtggaa gttagtgtt tagtttttt attagtgtg gtgtgttta 360
 ttttagtag taggtgtttg agtattgtt tattaatatt ggggttttag ggatttgaa 420
 tgttatgttg gataaattag aggttaattg ttgggtattt ggggtgggtg tgttgaatt 480
 tgtgtgtgtt tttgtgttg ggggtgttaa agtgtttga tgttttgtt taagtgttg 540
 tgttttttg ttgggttaa agggagggtg ttatagatg taagtttta ttttttta 600
 atttgtgat ttgtattt gtgtattgaa gattttatt tgtttgtat gttttttt 660
 tttttgta agtaattatg tttttgaaa tgggaaaggg alataatgt ttggttggtt 720
 tttttgggt ggggttttga aatgtttt ggttagtata tgggtggga gtatttgtt 780
 tgagtttat tttttatt tttttgtt ggttttagg aggtttgat gttagttagg 840
 tattaatgg taagaggatg aggatgtgt ttattgtat gtaattttg gagggtgaga 900
 gagaatttt tttaaatg tattgtttt gatttggag gattgaaatt gttattatt 960
 tgaatttgtt ggagaagtag gtgaaattt ggttttagaa ttgtgagt aagtataaga 1020
 aggaggggaa ggttatgtag aggaatagt atgtgggtt taagtgtgt gggagttagg 1080
 tgtattatgt gtgttttag gatgaggatt tttgttgtt ggttttagt aatgatata 1140
 aggagattt tttttatga gggaggggtt ttttttat atttttgtt ttggttagt 1200
 taggttaagt taaggtgttg ggtatttag ggttagaatt ttgtttat gtatgtgtt 1260
 tatttgaga agaaatgaat ttggaagtt tggaaatgat aagttgggtt ttgattttt 1320
 gtgtttttt ttgatttgt ttatttaga tttaatttg aagttataga ttttttaa 1380
 aaatgtaaat aatttataat ttaatttat ttgttgtat aatagaggaa aaatagggtt 1440
 ggtttaagtt taatattgta tgggttttt gaaagtatat gttagtatt tattttatt 1500
 ttttttaga attgataag aatataggat ttattgatta tttttgtt ttgttttaa 1560
 ataaaaatat ttaagtgaa aataatttag aaaattagat ttgtagggt ttgttttg 1620
 aaatttgtt tggggagaat taaaaatta agttgttga agttttttg tatgtgaata 1680
 ggtttatata aaatttat ttatattat ttaataaat gaaataaaaa ttagaattt 1740
 aaatttgtg tgtttttt ttattttt tttgtttt tttttaatg tttagagaaa 1800
 ggtatatga ggaanaagt gtttaggaa tttaggaaa atgttagta agaatttgtt 1860
 aatgtgggtt tttagtga gggagtgtt ggttaattg gtttttatg taatagaatt 1920
 ttgttaagg agatatttt agttatgat gttttatta ggtagtgtt ttattttt 1980
 aaaataggta attttttt agttgatag ataaattat ttatttgaa tgatattgat 2040
 tattaatgat aggtaaatt ttatttaga aggaagggt aaaaatttt attagtatt 2100
 tgtttttt ttattttt ttattttt ttatgtgaa aattgaatt atgtgaagga 2160
 attgtagag ttagaatagt tttaggaaga gtaataatt attaaatagg ttagaagtaa 2220
 atagtggaaa ttaataatg atgtataag tagaattagt gggttttt taatgttaag 2280
 aaaataaaaa gttagggata ggaagtatt tgtttaaga ttat 2325

<210> 245

<211> 2325

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 245

ataaatTTTT gaatagaata tttttgtt ttgaTTTT gtttttaa tttgagggga 60
aatttgttaa tttgtttgt agtatgtta ttaagtttt attgtttgt ttgatttgt 120
ttgatggatt gtgttttt ttaaaattat ttgatttta taaatttt tatataatt 180
aagttttgt attgagagaa atgaggaagt agaaagaaga aaataaaaat tagatggggg 240
attttatt tttttgtta aataaagggt tttttgtgt taatgggttag tgtatttta 300
aatggagtga ttgttttat taattgtgag gaggttgttt attttaagga tggagaggta 360
ttgtttgga gatgttata tgaataaagg tgttttttg gtgaaagtt ttgtatatag 420
aaaatttat gagttataaa ttttttagt taagagatt atattattaa gttttatt 480
aatattttt ttgaatttt tagatagtt tttttgtat atgttttt ttgatattg 540
gaggaggggg taggagaaga tagggagagt aaatattata gattaaaa tttgtttt 600
gtttatttta tttaaatata tatataata aattttat aaattttt atataataag 660
ggatttttag tgaattagat ttaaaattt tttaggtga aattttaga agtaagatt 720
ataaggttta attttttaa ttattttta ttgggtgtt ttgtttgaa aatgataata 780
gaaaaaat aataaattt gtgttttat tgaattttga aagagagtag ggaatgggga 840
ttgatattg ttttaaaaa ttatatag tttaaaatt aaattaat ttgttttt 900
ttgtatatg ataagaatga gttgaattat aggtatttta ttttttaa aaaaattgt 960
aatttaaagt tggagtttta gataaatagg ttaagaagga gatgtgaagg gtaggttt 1020
ggttgttta tttagaatt tttaggtttg tttttttt agatgggatt attgtaatga 1080
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gggatgtgag ggaggaggt tttttata agggggaaat tttttgtta ttgtgttg 1200
aggttgtga tagggaggt ttattttg agtgtgtga gtgtattgg ttgtattg 1260
attgtagt ttgtgttg tttttgtg tttttttt tttttttg tttttatt 1320
gggtgttg aaattagatt ttatttgt ttgttatag gtttaggtta gtgtgatt 1380
taattttg gagtgagat aggtatatgt tggagagaa tttttttt agtttagga 1440
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agttttgt ggaattgtga agagagggtga gagaggtaag gttgggtta ggtgttta 1560
tttatgtt taattagat gtttttagg gattttttg ggaagttta gttgaatt 1620
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aaatgtaag atgttttag ttgtttgat tggggatgt atataagtt aaatatatt 1860
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gttttagt taataagga atatttagt attttatt aggttaaaa tgtattagt 1980
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tggaggtga aagttgtt taggagtgt aaaggtgtg agttaggtt ttaagatt 2160
ttgtttat taagtgagg tagtggaatt ttgtgggt ttgtattg taggtgtg 2220
tggttagat aggtgtgtg ttgtgtgtt gtttaaggt ttgtgtgtt gttgtgtg 2280
ttgttgtt ttgttgtt gtgttgagt taggtgtg gggt 2325

<210> 246

<211> 2541

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 246

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tattgaaaa ttaaatata gaagaaaaa ttaattatt agaaaatt gtaaatatt 120
gagttatata aattgatat ttttaaaata tttaaatagt aataaattat gataattgt 180
taaggtttaa gttgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtatttt 240
gtagggttaa agtttagaag aatttatatt gaaatgtga aagttattg gtaagggtt 300
ttgggttta gaggttttg atgattgtaa ttatttgtt tttaattg aatgtttt 360
tttatatt tatatgatta ttttgaata aaaaaataa aagagtatgt tttttttt 420
tttagggag gttaggttta ggtgttatt aagggttgt ttgtatagt tagggaaagt 480
tagaatgga ggtatggag ttggggagg ggtttaatt aggttgtt ttgtttta 540

gaaagagtag ggggttag tgaagttat agagtttt gtgggtgta tgggtgtt 600
 ttaggttt atttttt ttgttatgg ttgttatg ttmtat tgggtgtg 660
 gggatatgg gaggtttt gggtttta atttttt ttaattta gtttaggt 720
 ggttttag gatttagt ttgttttg tgggtggg ttattgta ggatttagt 780
 ttgggttt ttgttggg tttaggtt tgggtttat gaattagtt ttgtattg 840
 ggaggttag gtgggagaal tattgaalt tgggaggtgg aggttagt gagtgagat 900
 tgtttatg tttttagt tgggtgata agtgagatt tgtttaat aaataataa 960
 ataaatagta gtaataatt ttgaggtt tttaggtt aggttgggg tagtttatg 1020
 taattttta gtaatttgg gaggtagga ttattgta ttgtttt tgatttaga 1080
 gataagaaat taagatttag aatataaga attgtttta ggttaaggag aagtggaggt 1140
 gtggggagga aataagta ttgatatta gagttatgt ttttaatt taagtggg 1200
 attttgat aaatttgt ttgttgta ttgggaag atttttt tttaggta 1260
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 gtttagaaa taggtatt ttgttata attttgtt tttttgtt gttttt 1560
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 ggagtttg tgggagaal tgaatttgg agttttga gttttgag ttittgagt 1860
 ttagtggg gtagtttt ttgttggg agttatgt tttagagt ttgaaatt 1920
 attgttga ggagtggt tgggtttt ggttaggta gattttgt agtttagt 1980
 ttgaaatga ggttggtga gattttt gggagtag aggtgggt ttgtttgt 2040
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 agtttaagt atttagtg gttgtagt tttagtgg gtaaggta gtgggtaga 2340
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 ttaagtatt gttatgtt atggatata tagagtga ggagattt tttttggg 2460
 atttagtt gtttagag gtgtttt agtagttg ttgtggg gatagtggt 2520
 ttgtttg tttagtt a 2541

<210> 247

<211> 2541

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 247

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 tagtatagg taggtattg gttattaag agtgagag ggtgagtag ttaggtagt 180
 attgttgg tgaaggttt tttagatta ttattttg ttagttta gaatttag 240
 ttgttggg tgtttggat tttaaaagt ttgggaatt tttaagggt ttatagta 300
 ttttttag ttaagtggg aagagttag gtttttgg ggttgggt tatalggt 360
 ttatagatt gtttgagag ggtgtgtt gttttgta tagtttat attgttagt 420
 gtgtttta ttgttat ttgtttg ttgtttt ttmttat ggttttgg 480
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 ttgttaatt ttgtttg ggttgggt ttatagaagt ttaattgt tgggtgtt 600
 gtaataatt ttgtgttg tgaatttg gttttgag agtttggat ttgttggg 660
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 gtaaatgat ttaggtta gattgttt gttaggatt tgggtgtg tgggttagg 900
 gttttatgg agttgtgt aatttggg gtgggttg ttgttgg ttatggaaga 960
 gaaaatgag gttgataag agaaaggat tagtgaagg gatgtatga ttgtattg 1020

gggattattt gtttttggg tttttgatt ttatttgg ataggggaaag gttttttg 1080
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 agtttaggtt ttgtataatt taatatttat taatatttt taataattta atgtttttt 2460
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<210> 248

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 248

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 tttttttt ttaaaattt taattgttt tattaagggt ttggataat tttagagatt 2400
 ttgtggaag ttgaaataa atttttga gatttgata attgtattag tttaggatt 2460
 taattggaat agaattaaaa ttttaaaat aagttttat a 2501

<210> 249

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 249

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 aaattttgt gaaatagatt aggaatttg gaaaggaaat aatgtgaga ttgttagat 180
 taaattatga gatttttaat ataatttta atattaatgt aataaaatt aaatttgg 240
 gtaataaaat tataaattt aatattggt ttaagtatag agaaaaagta tattatgtt 300
 gaattgtgaa aatattatt ttaaaatata gttgattaaa aaattgttg ggaattgatt 360
 ataattatg ataatttta agaaatatag atattaaaat attatttta tttttaat 420
 agaaattgt taaattataa ttaataaag gaggtataa aattttat ataatattg 480
 atatatatt ttggaaaaat atgtgtaatt gtttgttaa atatatgatt aattagtgt 540
 tgtgatgga taattatga gttttaat ttttgttt tttgtatt tttatagta 600
 ttgatgata tttttgtg ttaaaagtaa tttttaaag tttataatg ttgtaataa 660
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 ttatttgg ttgttttt agattttt tttttatt gggtgggatt tttgtgat 780
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<210> 250

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 250

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 ggggtaggag agttaggagg ggtgtatagt tgggttgagg tgggagtggt ttttttga 180
 aaggtagggg ggggtgtttt gtgtgatgg tggaggttat ttgtttgtg ttattatgg 240
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 ttaagaattg tgagggtttg ttattagggt ggtttttag ttgtgtatt ttgtagggg 360
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 gttgttttt atgtatttat agaaaaggta ggggtgaggta gttgaggtt ttaaggatt 480
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<210> 251

<211> 2257

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 251

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ttagttggg ttttttgt ttutggaat tagttgggt tttttatt ttgggagta  180
gtttgggtt ttatatatt tgggatgggt ttgttatt tagtttagta gtttttng  240
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gaggatatt tgggtgttag gtttttag gggaaattt gggatagta tatgtttat  720
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<210> 252

<211> 2434

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<220>

<221> unsure

<222> (1598, 1841, 1846, 1848, 1869, 1871, 1873, 1874, 1878, 1880)

<223> unknown base

<400> 252

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<210> 253

<211> 2434

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<220>

<221> unsure

<222> (555, 557, 561, 562, 564, 566, 587, 589, 594, 837)

<223> unknown base

<400> 253

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<210> 254

<211> 2476

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 254

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<210> 255
 <211> 2476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 255

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<210> 256

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 256

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<210> 257

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 257

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<210> 258

<211> 2555
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 258

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<210> 259
<211> 2555
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 259

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<210> 260

<211> 2516

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 260

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 atttattata taaaattaaa gataaaagt atattattat ttaattgat gtataagagg 180
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 ggaaatatt ttttgaaaa ttagtataag ataagggtt ttttttat ttttttat 360
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 atggatgaga tggagatt tgggttaag agtaatga atgattgt gttgagt 2040
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 agtttaggt ttgatatt atggattt tttatttg tttgttt ttttttag 2400
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 gaaatgaaa tatattat gttatgat aggaagatt aatattata aatgg 2516

<210> 261

<211> 2516

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 261

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 taagatagag ataggagtag tatattgtg gtttaggtg ggaggtggg tgaattatt 240
 gtagggagggt gtaagggtt ttttagtg agtgataat tggggggga aagtgggga 300
 tagtgtgat agtaagatg tttggaggt tagatattt tggtttgg attgtgtt 360
 ttgttttt atttagtg taagtattt tttgggtt ttgggttt taattttt 420
 tttatttg tgaatttt attttttt tgggttatg agtttggta ttgtgtat 480
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<210> 262

<211> 2364

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 262

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 taagagttaa gtttaggtgt gttataggtt gaaatataaa tgttaagggt ttataagga 180
 gttttatgg taggttaaga gtttttatt ttttgttg ttttgtt tttttgaga 240
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 ttttataaa ttaggaaaag atgatttagg agaaaaatag gtaaaaagt ttatagata 720
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 attagaaat tgttaattg ttgggtgtg tggtttatat ttgtaattt agtatttgg 840
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<210> 263

<211> 2364

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 263

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 gagttaatt ttgttttg tattggaagt gaattgattg tatatatagt ttgtttata 180
 tatatatgt ttitttgaa gtattagt tgaagagt ttagaatgt ataggagaga 240
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 ttittgata ttatgttat ttatattt tttatttt attggagta ttgttaagt 360
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<210> 264
 <211> 2408
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 264

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<210> 265
 <211> 2408
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 265

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<10> 266

<11> 2523

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 266

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<210> 267

<211> 2523

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 267

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 gtgttgatt tttttgt gtttagatt ttttalaag gtgtgggtg ttgttttg 240
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<10> 268

<11> 2280

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 268

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<210> 269

<211> 2280

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 269

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<210> 270
 <211> 2413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically treated genomic DNA (Homo sapiens)

<400> 270

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<210> 271
 <211> 2413
 <212> DNA
 <213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 271

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<210> 272

<211> 2171

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 272

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<210> 273

<211> 2171

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 273

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<210> 274

<211> 2490

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 274

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<210> 275

<211> 2490

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 275

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<210> 276
<211> 2418
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 276

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<210> 277
<211> 2418
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 277

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<10> 278

<11> 2351

<12> DNA

<13> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 278

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<210> 279

<211> 2351

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 279

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 atttagtt ttgttttt gttgaagt ggttaagt ttggatttt gtggatgt 240
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 ggaattgtt atggggtaa ttgttagg gagggtgga gaaggagg tttagtagt 360
 ttgttgtt ttatgaaga aggaaggagg ttgttaatt ggtgttagt ttgttat 420
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<210> 280

<211> 2427

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 280

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 tttttggg taggaggggt tatttggta gggtaaaaag agataaalag aaaaataata 180
 gtaataata tagtaataat ttgggttgt tttatggg ttgtttga ataggttgt 240
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 ggatagta gtattggt tgtgtgtg gggattgg ttgttagg tttagtgg 360
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 ggaattgggt ttgtgaatt gtttagggat ggggaaggag taggtgagg tatggggt 480
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 tattaaaa ataaaaaaa aaaaaaaat tagtgggt tgggttagg tattgtagt 960
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<10> 281

<11> 2427

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 281

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 gtagtattt tttagaag tgggtgtta gtgttgtt gattaggtt tgggttatt 480
 agagttagt agagagggtt gaagtgggt tggggagggt gaggagggtt tgttggat 540
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 ttgtttagg atgggttga gatttttag ggttgggtt ttttttat aaggaggaa 720
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<210> 282
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 282

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<210> 283
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 283

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<210> 284

<211> 3190

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 284

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<210> 285

<211> 3190

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 285

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<210> 286

<211> 2613

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 286

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<10> 287

<11> 2613

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

<400> 287

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<10> 288

<11> 2501

<12> DNA

<13> Artificial Sequence

<20>

<23> chemically treated genomic DNA (Homo sapiens)

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<210> 289

<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 289

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<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 290

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<211> 2501

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 291

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<210> 292
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 292

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<211> 2501
<212> DNA
<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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<210> 294

<211> 6009

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

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<223> Detection primer for

<400> 301

caaaataacc aatcccctaa a

21

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<223> Detection primer for LIM/HOMEBOX PROTEIN LHX9

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23

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<223> Detection primer for LIM/HOMEBOX PROTEIN LHX9

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<223> Detection primer for

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ttaatgaagt agggtttgta ttgt

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<223> Detection primer for

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cccaactaac tcaaattcca c

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gtggtttgg ggaattagta t

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<223> Detection primer for

<400> 309

ctcctacata tcccatctca tc

22

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<223> Detection primer for UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR
(UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN
UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1)
(GMP1) (SENTRIN)

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<223> Detection primer for UBIQUITIN-LIKE PROTEIN SMT3C PRECURSOR
(UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN
UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1)
(GMP1) (SENTRIN)

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<223> Detection primer for BASSOON; ZINC FINGER PROTEIN 231; NEURONAL
DOUBLE ZINC FINGER PROTEIN

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<210> 313

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<212> DNA

<213> Artificial Sequence

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<223> Detection primer for BASSOON; ZINC FINGER PROTEIN 231; NEURONAL
DOUBLE ZINC FINGER PROTEIN

<400> 313

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<210> 314

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<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for BASSOON; ZINC FINGER PROTEIN 231; NEURONAL
DOUBLE ZINC FINGER PROTEIN

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<210> 315

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<220>

<223> Detection primer for BASSOON; ZINC FINGER PROTEIN 231; NEURONAL
DOUBLE ZINC FINGER PROTEIN

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<400> 316

ttgtgttgtg tgtaaaagga

20

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<212> DNA

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<400> 317

caaacactat acacctctca aca

23

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<223> Detection primer for

<400> 318

ttgaggttat tggttatag atttt

25

<210> 319

<211> 18

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ccctaaccac cccttcta

18

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tgtgtgaaat gtttagttt aattg

25

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<223> Detection primer for HOOK2 PROTEIN

<400> 322

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21

<210> 323

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<223> Detection primer for HOOK2 PROTEIN

<400> 323

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<210> 324

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<220>

<223> Detection primer for

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ggttgggatt ttagtgtgtg

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<210> 325

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<213> Artificial Sequence

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<223> Detection primer for

<400> 325

aattacaaa ccaattcctc tta

23

<210> 326

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<212> DNA

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<220>

<223> Detection primer for

<400> 326

ttatttgagg gatttattgg ag

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<210> 327

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 327

ccttataaaa acttaccacc ctat

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<210> 329
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<223> Detection primer for LYSOSOMAL-ASSOCIATED MULTITRANSMEMBRANE PROTEIN
(RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5

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<223> Detection primer for "TYPE I INOSITOL-1,4,5-TRISPHOSPHATE
5-PHOSPHATASE (EC 3.1.3.56) (SPTASE)

<400> 337

atcccaacaa cttcttctc 20

<210> 338
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Detection primer for PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE
(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

<400> 338

gaagaggaat gggaaaatta g

21

<210> 339

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE
(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

<400> 339

tcaccaacaa aatacccaa

19

<210> 340

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE
(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

<400> 340

tgagtaagat gattatttgg attt

24

<210> 341

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE
(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

<400> 341

aaccatcaac catacctatt tc

22

<210> 342

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 342

atggggttg aaagagttgt ag

22

<210> 343
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 343

cacttccac ctccttatat c

21

<210> 344
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 344

atgatgggaa tatgtaagaa tga

23

<210> 345
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 345

cttctcacta ctaatctcct accc

24

<210> 346
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1
(EQUILBRATIVE NITROBENZYL MERCAPTOPURINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR-SENSITIVE NUCLEOSIDE
TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE)

<400> 346

gagttggagg gttttgttt a

21

<210> 347
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1
(EQUILBRATIVE NITROBENZYL MERCAPTOPURINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR-SENSITIVE NUCLEOSIDE

TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE

<400> 347

caaaactcca taaaattcat ct

22

<210> 348

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

<400> 348

gtgtgagggt tgggtatttt t

21

<210> 349

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

<400> 349

ccactcactc aaccataa

19

<210> 350

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC
3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR)
(IAR) (PHOGRIN)

<400> 350

gatgtgggt agtgtgttt at

22

<210> 351

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC
3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR)
(IAR) (PHOGRIN)

<400> 351

aaaacctatc tacaccttc tctt

24

<210> 352

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 352

aattagagaa ggtaaattgg gtt

23

<210> 353

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 353

attccccacca aaacctctac

20

<210> 354

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 354

gggatttggg aatttattgt

20

<210> 355

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 355

aataactcca acttcctcc c

21

<210> 356

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 356

ggtggatgag tagttgaag ttt

23

<210> 357
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 357

aaaaaccct tccctct

18

<210> 358
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 358

gttggtgtt agtaattgaa aa

22

<210> 359
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for

<400> 359

accaacacaa actaacactt acat

24

<210> 360
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14)
(PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING
PROTEIN)

<400> 360

aagaggttt atggtgttg ag

22

<210> 361
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for PEROXISOMAL MEMBRANE PROTEIN PEX14 (PEROXIN-14)
(PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1 RECEPTOR DOCKING
PROTEIN)

<400> 361

cactcccttc ccaaactata c

21

<210> 362

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2)

<400> 362

gtggaaaaag gagagtaaat tg

22

<210> 363

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2)

<400> 363

ctcctcaatt ctcacaaaa

20

<210> 364

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1)

<400> 364

agggagggtt ggtgtatatt

20

<210> 365

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for LIM DOMAIN KINASE 1 (EC 2.7.1.37) (LIMK-1)

<400> 365

aaaccctact tctacaaac aa

22

<210> 366

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION
RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR
II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 366

ggaaaggata ggatgttga t

21

<210> 367

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION
RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC RECEPTOR
II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 367

caatccctt aaaacaaacc

20

<210> 368

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE
GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3)
(LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT-GAMMA)
(1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 368

ttagggagat gagattaaag ga

22

<210> 369

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE
GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3) (1-AGPAT 3)
(LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA) (LPAAT-GAMMA)
(1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 369

cacaattcc cacaaaaca

19

<210> 370

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HOMEBOX PROTEIN GSH-2

<400> 370

tatatggggt gggagtattt t

21

<210> 371

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HOMEBOX PROTEIN GSH-2

<400> 371

ccttccctc ctcttatac t

21

<210> 372

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 372

ttaggggta ttaggttaa tga

23

<210> 373

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 373

aaaattctt cctctcctaa aca

23

<210> 374

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HISTONE H4

<400> 374

ttagtgaga aagtgggggt

20

<210> 375

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for HISTONE H4

<400> 375

ctacctcaaa ccaaaatcct c

21

<210> 376

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT
MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2)

<400> 376

ttttggagtt atagggtttt gt

22

<210> 377

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT
MEMBER 2 (NEUROBLASTOMA- SPECIFIC POTASSIUM CHANNEL KQT-LIKE 2)

<400> 377

cttcaacatc tcccaatcc

19

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B
SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B
SUBUNIT) (GOLGI ADAPTOR HA1/API ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN
ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT
OF AP-1 CLATHRIN).(DC22)

<400> 378

gggttatgtt aaggagaaa g

21

<210> 379

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1B
SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B
SUBUNIT) (GOLGI ADAPTOR HA1/API ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN
ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT

OF AP-1 CLATHRIN) (DC22)

<400> 379

aaacctaata atccaacaca aa

22

<210> 380

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 380

atttgtagta gttataggt atgttta

27

<210> 381

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 381

aataaccta tctccaaacc c

21

<210> 382

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 382

tagagaagtt gttgttggt tg

22

<210> 383

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 383

taccaccat ataccaaaac taaa

24

<210> 384

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PERIPLAKIN (195 KDA CORNIFIED ENVELOPE

PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN)

<400> 384

attgagggg tattattgt tg

22

<210> 385

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PERIPLAKIN (195 KDA CORNIFIED ENVELOPE
PRECURSOR) (190 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN)

<400> 385

aaccaccttc tccccta

19

<210> 386

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 386

gtaataattg ggtaggggt ta

22

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 387

aaccaatc aaataactaa aatcc

25

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 388

tattgagaa agtgtagga gg

22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 389

aaaatccaat cctaaaaccc ta

22

<210> 390

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 390

tttatgttg ttggggtag t

21

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 391

aaccctaact tctaaacaat tcc

23

<210> 392

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 392

gtgagagtgg gtgtgaaat

20

<210> 393

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 393

acccaatca actacataac taa

23

<210> 394

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 394

gaaggtagg tagtaagaag ggt

23

<210> 395

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 395

tacctaattcc cccaaaaca

19

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 396

ggaggagttg ggagtagta t

21

<210> 397

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 397

cactcactta atcatcacca tc

22

<210> 398

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 398

tgatttgatt agtttggtat tgtt

24

<210> 399

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 399

caaacacccc ttaaccct

18

<210> 400

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 400

tagtgtgtt ggtagagtg gt

22

<210> 401

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for

<400> 401

acacatctta aactcccca

20

<210> 402

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for DNA REPLICATION FACTOR; DOUBLE PARKED,
DROSOPHILA, HOMOLOG OF

<400> 402

gttgggttta tttgagttg ag

22

<210> 403

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for DNA REPLICATION FACTOR; DOUBLE PARKED,
DROSOPHILA, HOMOLOG OF

<400> 403

aaccaacacc tcctaaacaa t

21

<210> 404

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION

FACTOR MEL1)

<400> 404

ngtttggtt tgagtaagaa gg

22

<210> 405

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for PR-DOMAIN ZINC FINGER PROTEIN 16 (TRANSCRIPTION FACTOR MEL1)

<400> 405

ataccccaat aaccacctct at

22

<210> 406

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN

<400> 406

ggtattagga ggtagaagtg ga

22

<210> 407

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for TUMOR SUPPRESSING SUBTRANSFERABLE CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN

<400> 407

accaatctaa aaatccccaa c

21

<210> 408

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for CDH1

<400> 408

gagggtgggg ttagaggat

19

<210> 409

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for CDH1

<400> 409

caaactcaca aatactttac aattc

25

<210> 410

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for CD44

<400> 410

gaaaggagag gttaaagggt g

21

<210> 411

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for CD44

<400> 411

aactcactta actccaatcc c

21

<210> 412

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection primer for GSTP1

<400> 412

gttggtttta tgttgggagt t

21

<210> 413

<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for GSTP1

<400> 413

cctctcccct accctataaa 20

<210> 414
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for VIAAT

<400> 414

gaagttgttg tatatgaggt tgta 25

<210> 415
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for VIAAT

<400> 415

caaacccaat tctcaatc c 21

<210> 416
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 416

tagacgcgga cgttta 16

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 417

taattagatg tggatgtt 18

<210> 418
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 418

ttcgtatagg tacgcga

17

<210> 419
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 419

ttttgtatag gtagtga

18

<210> 420
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 420

ttcgtacgcg tattat

16

<210> 421
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 421

gagttttgta tgtgtatt

18

<210> 422
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for VIAAT

<400> 422

ttcggtcgtt tagcgt

16

<210> 423

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for VIAAT

<400> 423

atttggttgt ttagtgt

17

<210> 424

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 424

gtcggtggtt cgagta

16

<210> 425

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 425

gttggtggtt tgagtat

17

<210> 426

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 426

ggaattcgac ggggag

16

<210> 427

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 427

gggaattga tgggga

16

<210> 428

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 428

ttcgtcgggc gttag

16

<210> 429

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 429

ttgttggt gttagt

17

<210> 430

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 430

gtcgttcgtc gatgta

16

<210> 431

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 431

ggttgttgt tgatgtag

18

<210> 432

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 432

gtattgcgcg ttatt

16

<210> 433
<211> 17
<212> DNA
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<220>
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<400> 433

agggtattgt gtgttta 17

<210> 434
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<212> DNA
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<220>
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<400> 434

aggtagtgg cgtttt 16

<210> 435
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for

<400> 435

aggtagtgg tgtttt 16

<210> 436
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
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PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5

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16

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16

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16

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16

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16

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PROTEIN (RETINOIC ACID- INDUCIBLE E3 PROTEIN) (HA1520) LAM5

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5-PHOSPHATASE (EC 3.1.3.56) (SPTASE)

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16

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5-PHOSPHATASE (EC 3.1.3.56) (SPTASE)

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16

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5-PHOSPHATASE (EC 3.1.3.56) (SPTASE)

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<210> 589

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5-PHOSPHATASE (EC 3.1.3.56) (5PTASE)

<400> 589

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5-PHOSPHATASE (EC 3.1.3.56) (5PTASE)

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5-PHOSPHATASE (EC 3.1.3.56) (5PTASE)

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5-PHOSPHATASE (EC 3.1.3.56) (5PTASE)

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17

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<223> Detection oligonucleotide for PROSTAGLANDIN E2 RECEPTOR, EP4 SUBTYPE
(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

<400> 594

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16

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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<210> 602
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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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16

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(PROSTANOID EP4 RECEPTOR) (PGE RECEPTOR, EP4 SUBTYPE)

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(EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPT-SENSITIVE NUCLEOSIDE
TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE)

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17

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(EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR-SENSITIVE NUCLEOSIDE
TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE)

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18

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<223> Detection oligonucleotide for EQUILBRATIVE NUCLEOSIDE TRANSPORTER 1
(EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR-SENSITIVE NUCLEOSIDE
TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE)

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17

<210> 633
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(EQUILBRATIVE NITROBENZYL MERCAPTOPYRINE RIBOSIDE-SENSITIVE
NUCLEOSIDE TRANSPORTER) (EQUILBRATIVE NBMPR-SENSITIVE NUCLEOSIDE
TRANSPORTER) (NUCLEOSIDE TRANSPORTER, ES-TYPE)

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<210> 634
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<223> Detection oligonucleotide for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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16

<210> 635

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<223> Detection oligonucleotide for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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18

<210> 636

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(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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16

<210> 637

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(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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17

<210> 638

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<223> Detection oligonucleotide for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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16

<210> 639

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<223> Detection oligonucleotide for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

<400> 639

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16

<210> 640

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<223> Detection oligonucleotide for ORPHAN NUCLEAR RECEPTOR NR5A2
(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

<400> 640

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16

<210> 641

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(ALPHA-1-FETOPROTEIN TRANSCRIPTION FACTOR) (HEPATOCYTIC TRANSCRIPTION
FACTOR) (B1-BINDING FACTOR) (HB1F) (CYP7A PROMOTER BINDING FACTOR)

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17

<210> 642

<211> 16

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<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

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16

<210> 643

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<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED

PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 643

ttgtttgat tgaagg

17

<210> 644

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 644

aggcgatcga tattag

16

<210> 645

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 645

ggtgattgat attaggg

17

<210> 646

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 646

ttagcggtcg tcgtta

16

<210> 647

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 647

taattagtgt ttgttgta

19

<210> 648

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 648

atcggttcgg gaattt

16

<210> 649

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PROTEIN-TYROSINE PHOSPHATASE X
PRECURSOR (EC 3.1.3.48) (R-PTP-X) (ISLET CELL AUTOANTIGEN RELATED
PROTEIN) (ICAAR) (IAR) (PHOGRIN)

<400> 649

agattggttt gggaat

16

<210> 650

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 650

gtcgatttcg ttacgg

16

<210> 651

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 651

gttgattttg ttatggg

17

<210> 652

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 652

ttcgggttc gtatta

16

<210> 653

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 653

ttttgggtt tgtattag

18

<210> 654

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 654

aattcgcggt ttcgat

16

<210> 655

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 655

aatttgtgtt ttgatg

17

<210> 656

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 656

gtcgttcgc ggagat

16

<210> 657

<211> 17

<212> DNA

<213> Artificial Sequence

<20>
<23> Detection oligonucleotide for

<400> 657

gttgtttgt ggagatt

17

<210> 658
<211> 16
<212> DNA
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<20>
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<400> 658

attggtcgat tcgcgg

16

<210> 659
<211> 17
<212> DNA
<213> Artificial Sequence

<20>
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<400> 659

tattggtga ttgtgg

17

<210> 660
<211> 16
<212> DNA
<213> Artificial Sequence

<20>
<23> Detection oligonucleotide for

<400> 660

agcgttcga ttctgg

16

<210> 661
<211> 17
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<20>
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<400> 661

agtgtttga ttgtgt

17

<210> 662
<211> 16
<212> DNA
<213> Artificial Sequence

<20>
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<400> 662

atcgagcgtt tcgatt

16

<210> 663

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 663

ggattgagtg tttgat

17

<210> 664

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 664

attcgcgtat tcgaga

16

<210> 665

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 665

tttgtgtatt tgagagg

17

<210> 666

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 666

gacgttcgcg attaaa

16

<210> 667

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 667

tgatgttg tgattaa

17

<210> 668

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 668

aagtcgatat cgcggt

16

<210> 669

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 669

aaaagttgat attgtggt

18

<210> 670

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 670

agcgttcgga agttta

16

<210> 671

<211> 16

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<213> Artificial Sequence

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<223> Detection oligonucleotide for

<400> 671

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<210> 672

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 672

tattcggacg gggata

16

<210> 673
<211> 16
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<220>
<223> Detection oligonucleotide for

<400> 673

atttggatgg ggatag

16

<210> 674
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<220>
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<400> 674

gagacgcgta ggttat

16

<210> 675
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<213> Artificial Sequence

<220>
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<400> 675

gggagatgtg taggtt

16

<210> 676
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<220>
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<400> 676

tagtttcgg cgaagg

16

<210> 677
<211> 17
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<220>
<223> Detection oligonucleotide for

<400> 677

ggtagttttt ggtgaag

17

<210> 678

<211> 16
<212> DNA
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<220>
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<400> 678

aaggcgggtga cgtaaa

16

<210> 679
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<220>
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<400> 679

aaggtggtga tgtaaa

16

<210> 680
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<220>
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<400> 680

atggcgtaag tacgtt

16

<210> 681
<211> 17
<212> DNA
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<220>
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<400> 681

gatggtgtaa gtatgtt

17

<210> 682
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
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<400> 682

agtacgttcg ggacga

16

<210> 683
<211> 17
<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 683

aagtatgtt gggtga

17

<210> 684

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 684

atggtattcg ggtcgt

16

<210> 685

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 685

tatggtattt gggtgt

17

<210> 686

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 686

ttggagcgtt aagtaa

16

<210> 687

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1

RECEPTOR DOCKING PROTEIN)

<400> 687

tatttgagtg gtaagta

18

<210> 688

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 688

tgaaagattc gtttgtt

17

<210> 689

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 689

gtgaaagatt tgttgtt

18

<210> 690

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 690

tgtataacga gaggtg

16

<210> 691

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 691

tgtataatga gaggtga

17

<210> 692

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 692

atgtttcggg tatgga

16

<210> 693

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for PEROXISOMAL MEMBRANE PROTEIN PEX14
(PEROXIN-14) (PEROXISOMAL MEMBRANE ANCHOR PROTEIN PEX14) (PTS1
RECEPTOR DOCKING PROTEIN)

<400> 693

atgttttggg tatgga

16

<210> 694

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 694

ttttcgagga attcgt

16

<210> 695

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 695

tttttgagg aatttgtt

18

<210> 696
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 696

atagtttcg gcgggt 16

<210> 697
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 697

tatagtttt ggtgggt 17

<210> 698
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 698

ttttcgcg tagata 16

<210> 699
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 699

tgtttttg ttagat 17

<210> 700
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 700

ttacgggcgt tagaga

16

<210> 701

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN HOX-B6 (HOX-2B)
(HOX-2.2)

<400> 701

ggagttatgg gtgtta

16

<210> 702

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 702

tatcggatta tcgcgg

16

<210> 703

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 703

attggattat tgtgggg

17

<210> 704

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 704

gtcggtagtt tatcgga

18

<210> 705

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 705

gttgtagtt tattgga

18

<210> 706

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 706

taggagacgt tacgtt

16

<210> 707

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LIM DOMAIN KINASE 1 (EC 2.7.1.37)
(LIMK-1)

<400> 707

agatgttatg ttagggt

17

<210> 708

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 708

aagaacggac gtgttt

16

<210> 709

<211> 16

<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 709

aggaagaatg gatgtg

16

<210> 710
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 710

ttttgcgat agtcgg

16

<210> 711
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 711

gtttttgtga tagttgg

17

<210> 712
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 712

tagcggcgat ttaagg

16

<210> 713
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 713

gtagtggtga ttaaagg

17

<210> 714

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 714

tttaggagcg agtcgt

16

<210> 715

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
REGION RECEPTOR II-A PRECURSOR (FC-GAMMA RII-A) (FCRII-A) (IGG FC
RECEPTOR II-A) (FC-GAMMA-RIIA) (CD32) (CDW32)

<400> 715

tttatgagt gagttgtt

18

<210> 716

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 716

tttcgatagt atacggg

17

<210> 717

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 717

tttgatagta tatgggga

18

<210> 718

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 718

aagggagcgt tcgtta

16

<210> 719

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 719

aagggagtgt ttgtta

16

<210> 720

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 720

aataatagcg acgggg

16

<210> 721

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSFERASE GAMMA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE 3)
(1-AGPAT 3) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE-GAMMA)
(LPAAT-GAMMA) (1-ACYLGLYCEROL-3-PHOSPHATE O- ACYLTRANSFERASE 3)

<400> 721

taatagtgat ggggggt

16

<210> 722

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 722

tttagaatcg tcgagt

16

<210> 723

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 723

agaattgttg agtgaag

17

<210> 724

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 724

ttttcgtcg gttcgta

17

<210> 725

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 725

ttgttggtt ttagga

17

<210> 726

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 726

aggacggcgt ttatta

16

<210> 727

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 727

gatgaggatg gtgttt

16

<210> 728

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 728

ttcgatttcg gaggat

16

<210> 729

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for HOMEBOX PROTEIN GSH-2

<400> 729

ttgatttg gaggatt

17

<210> 730

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Detection oligonucleotide for

<400> 730

ttcgtatcg agagtt

16

<210> 731

<211> 17

<212> DNA

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1B SUBUNIT (SIGMA-ADAPTIN 1B) (ADAPTOR PROTEIN COMPLEX AP-1 SIGMA-1B SUBUNIT) (GOLGI ADAPTOR HA1/AP1 ADAPTIN SIGMA-1B SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 SIGMA- 1B SMALL CHAIN) (SIGMA 1B SUBUNIT OF AP-1 CLATHRIN) (DC22)

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DROSOPHILA, HOMOLOG OF

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DROSOPHILA, HOMOLOG OF

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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(TRANSCRIPTION FACTOR MEL1)

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC TRANSPORTER-RELATED PROTEIN

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16

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16

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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16

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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CANDIDATE 5; P45 BECKWITH-WIEDEMANN REGION 1A; BECKWITH-WIEDEMANN
SYNDROME CHROMOSOME REGION 1, CANDIDATE A; EFFLUX TRANSPORTER-LIKE
PROTEIN; ORGANIC CATION TRANSPORTER-LIKE 2; TUMOR-SUPPRESSING STF
CDNA 5; IMPRINTED MULTI-MEMBRANE SPANNING POLYSPECIFIC
TRANSPORTER-RELATED PROTEIN

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<210> 884

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<210> 885

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gcgcatgcgg 10

<210> 940

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gcgacgtcgg 10

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gccgcgngng 10

<210> 942

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agcggccgcg 10

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ctcccacgcg 10

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<211> 10

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aggggacgcg 10

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gagaggcgcg 10

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gccccgcga 10

<210> 949
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<400> 949

cggggcgcgga 10

<210> 950
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<400> 950

ggggacgcga 10

<210> 951
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acccacccg 10

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agcactctcc agcctctcac cgac 24

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ccgggctcggt ga 12

<210> 954
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accgacgtcg actatccatg aacc 24

<210> 955
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ccgggggttca tg 12

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aggcaactgt gctatccgag tgac 24

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<400> 957

ccgggtcact cg 12

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cgcgctactc cgcataca 18

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gaggtaatcg aggcggtcg 19

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<210> 961

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<220>
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<400> 961

accgaaaata cgcttcacg 19

<210> 962

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<220>
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<400> 962

gcgttatcgt aaagtattgc gc

22

<210> 963

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cgcgacgaac aaaacgccg

19

<210> 964

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<400> 964

gcgttttacg tcgtcgcg

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<210> 965

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gacgctaaac gccaccgt

18

<210> 966

<211> 23

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<400> 966

ccgaccatcc gacgccttac tcg

23

<210> 967

<211> 25

<212> DNA

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<400> 967

cgaattata ccgaacgctc ctacg

25

<10> 968

<11> 22

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 968

aggttacggg aggtcgaggt cg

22

<10> 969

<11> 27

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 969

ccgccatcg accgttcccg accccta

27

<10> 970

<11> 20

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 970

tcccgaattt ataccgaacg

20

<10> 971

<11> 21

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 971

ttttatttag gggtcgggaa c

21

<10> 972

<11> 18

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acgccccgcc atcgaccg

18

<210> 973
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<400> 973

ttgtggttcg ggaagagac 19

<210> 974
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<400> 974

cttcgatcga aaaaaaccg 19

<210> 975
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<220>
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aactacgcgc aaacccgcga 20

<210> 976
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<400> 976

cgttttcgt ttattttcg c 21

<210> 977
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<400> 977

gacaaaaaac gccacgtc 18

<210> 978

<211> 22
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<400> 978

ccgacaattc accgaatcac cg 22

<210> 979
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<400> 979

atctcaccta ccgtcgcg 18

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<400> 980

taggagtgcg atcgttgc 19

<210> 981
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<400> 981

acgaacgtta cgaccgatac ccaacta 27

<210> 982
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<400> 982

aacgtatccc gacaatccg 19

<210> 983
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<400> 983

gagtatttaa ggtttagtga aacgttagc 29

<210> 984

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 984

caaataacgc gacactaac gcataattc 29

<210> 985

<211> 18

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<213> Artificial Sequence

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<223> chemically treated genomic DNA (Homo sapiens)

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tgttttcgga gtgcgttc 18

<210> 986

<211> 20

<212> DNA

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<223> chemically treated genomic DNA (Homo sapiens)

<400> 986

aatcaaacc gacgatacga 20

<210> 987

<211> 22

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<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 987

ccgataaaac gcgtccaaac cg 22